

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2000, 14:43:21 ; Search time 1282.56 Seconds
(without alignments)
3814.004 Million cell updates/sec

Title: US-09-206-132-1
Perfect score: 1120
Sequence: 1 CACAGGCGTAAGCTTGTCT.....AGAGTAAGCCCAAAAAA 1120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 218378903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Geneml: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_cm: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pl1: *
8: gb_pl2: *
9: gb_pr1: *
10: gb_pr2: *
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13: em_hum1: *
14: em_hum2: *
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17: em_or: *
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43: em_htg3: *

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88: gb_ro: *
89: gb_sts1: *
90: gb_sts2: *
91: gb_sy: *
92: gb_un: *
93: gb_v11: *
94: gb_v12: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Match Length	ID	Description
1	1120	100.0	1120	5 AR030780	AR030780 Sequence
2	1112	99.3	1112	83 HUMB72A	L25259 Human CTLLA4
3	995.8	88.9	1424	82 HSU04343	U04343 Human CD86
4	597	53.3	1897	3 AF106826	AF106826 Canis fam
5	567.2	50.6	1156	3 RABCD86B	D49842 Rabbt mRNA
6	537	47.9	994	3 PIGCD86G	L76099 Sus scrofa
7	534.8	47.7	1138	3 AF157827	AF157827 Felis cat
8	468.2	41.8	1795	3 AF106827	AF106827 Canis fam
9	407.2	36.4	984	88 AF065897	AF065897 Mus muscu
10	407.2	36.4	984	88 AF065898	AF065898 Mus muscu
11	407.2	36.4	984	88 AF065899	AF065899 Mus muscu
12	407.2	36.4	984	88 AF065900	AF065900 Mus muscu

VERSION	125259.1	GI:416368
KEYWORDS	CTLA4 counter-receptor.	
SOURCE	Homo sapiens cDNA for mRNA.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 1112) Freeman-G-I-T-Gibben, J.G., Bousfiotis, V.A., Ng, J.W., Restivo, V.A., J., Lombard, L.A., Gray, G.S. and Nadler, L.M.	
TITLE	Cloning of B7-2, a CTLA-4 counter-receptor that costimulates human T cell proliferation (see comments).	
JOURNAL	Science 262 (5135), 909-911 (1993)	
MDLINE	94053735	
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121 CACTATGGAGCTGAGTAAATCTCTTTTGATGAGGCTCCCTGCTCTGAGTCTCTCC	180	
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181 TCTGAAGATTCAAGCTTATTTCATGAGACTGCAGACTGCCATGCCAAATTTGCAAACT	240	
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Db	541	TAAATATACAGAAATGTGTACATAAATTTTGACTGCTCATCTATACAGGTTTACCCAGA	600
QY	601	ACCTAAAGAGTGGTGTGGTAAACCAACAAATTCACATTCAGATATGATGGTAT	660
Db	601	ACCTAAAGAGTGGTGTGGTAAACCAACAAATTCACATTCAGATATGATGGTAT	660
QY	661	TATGACAGAAATCTCAGATATATGTACAGAACTGTACAGCTTTTCATCAGCTGTCTGT	720
Db	661	TATGACAGAAATCTCAGATATATGTACAGAACTGTACAGCTTTTCATCAGCTGTCTGT	720
QY	721	TTTATTCCTCGATGTATACAGCAATATGACCATCTTCTGTATTTCTGGAACTGACCAAGAC	780
Db	721	TTTATTCCTCGATGTATACAGCAATATGACCATCTTCTGTATTTCTGGAACTGACCAAGAC	780
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Db	1021	AAGATCTGATGAGAGCCAGCGTGTTTTAAAAAGTTGGAAGCATCTTATGCGCAAAAG	1080
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Db	1081	TGATACATGTTTAAATTAAGAGTAAAGGCC	1112
RESULT 3	HSU04343		
LOCUS	HSU04343	1424 bp	mRNA
DEFINITION	Human CD86 antigen mRNA, complete cds.		
ACCESSION	U04343		
VERSION	U04343.1	GI:439838	
KEYWORDS	B70; B7-2.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Azuma,M., Ito,D., Yagita,H., Okumura,K., Phillips,J.H., Lanier,L.L.		
JOURNAL	and Somoza,C.		
MEDLINE	B70 antigen is a second ligand for CTLA-4 and CD28		
AUTHORS	Nature 366 (6450), 76-79 (1993)		
TITLE	2 (bases 1 to 1424)		
JOURNAL	Fernandez-Ruiz,E., Somoza,C., Sanchez-Madrid,F. and Lanier,L.L.		
REFERENCE	CD28/CTLA-4 ligands: the gene encoding CD86 B(B70/B7.2) maps to the		
	same region as CD80 (B7/B7.1) gene in human chromosome 3q13-q23		
	unpublished		
	3 (bases 1 to 1424)		

Query Match 50.6% Score 567.2; DB 3; Length 1156;
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 3'UTR /product="CD86"
 BASE COUNT 339 a 255 c 264 g 298 t
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QY 1070 TCGCAAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1112
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RESULT 7
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LOCUS AF157827 1138 bp mRNA MAM 08-MAY-2000
DEFINITION Fells catus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
SOURCE
cat.
Fells catus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 1138)
AUTHORS
Choi,I.-S., Hash,S.M., Winslow,B.J. and Collisson,E.W.
TITLE
Sequence analyses of feline B7 costimulatory molecules
JOURNAL
Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE
20180222
REFERENCE
2 (bases 1 to 1138)
AUTHORS
Choi,I.-S., Hash,S., Winslow,B.J. and Collisson,E.W.
TITLE
Direct Submission
JOURNAL
Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 Rm. 222, College Station, TX 77843, USA
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Db 1033 CAGCGACAAAGTGA 1048

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RESULT 8

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LOCUS AF106827 1795 bp mRNA MAM 14-DEC-1999
DEFINITION Canis familiaris truncated B7-2 protein (CD86) mRNA, complete cds.
ACCESSION AF106827
VERSION AF106827.1 GI:6572518
KEYWORDS
SOURCE
ORGANISM

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Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS Yang, S. and Sim, G.-K.
TITLE New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE 20039396
REFERENCE 2 (bases 1 to 1795)
AUTHORS Yang, S. and Sim, G.-K.
TITLE Direct submission
JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA
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gene
5'UTR
CDS

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RESULT 9
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LOCUS AF065897
DEFINITION Mus musculus strain A/J CD86 antigen (Cd86) mRNA, complete cds.
ACCESSION AF065897
VERSION AF065897.1 GI:4587839
KEYWORDS
SOURCE house mouse.

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RESULT 15
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LOCUS Murine B7-2 mRNA, complete cds.
DEFINITION L25606
ACCESSION L25606
VERSION 1
KEYWORDS GI:432478
SOURCE Mus musculus
ORGANISM Mus musculus CDNA to mRNA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1183)
AUTHORS Freeman,G.J., Borriello,F., Hodes,R.J., Reiser,H., Gribben,J.G.,
Ng,J.W., Kim,J., Goldberg,J.M., Hathcock,K., Laszlo,G.,
Lombard,L.A., Wang,S., Gray,G.S., Nadler,L.M. and Sharpe,A.H.
MURINE B7-2, an alternative CTLA4 counter-receptor that
costimulates T cell proliferation and interleukin 2 production
J. Exp. Med. 178 (6), 2185-2192 (1993)
JOURNAL MEDLINE
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Matches 581; Conservative 0; Mismatches 263; Indels 6; Gaps 1;
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Search completed: November 5, 2000, 23:47:22
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: US-09-206-132-1
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1014.8	90.6	1161	6	PCT-US94-09642-24
6	995.8	88.9	1428	6	PCT-US94-09642-1
7	407.2	36.4	1151	3	US-08-456-104-3
8	407.2	36.4	1151	6	PCT-US95-02576-20
9	407.2	36.4	1151	6	US-08-479-744A-22
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11	325.2	29.0	330	5	US-08-479-744A-44
12	306	27.3	306	5	US-08-479-744A-46
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22	39.6	3.5	627	2	US-08-455-416-23
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ALIGNMENTS

RESULT 1
US-08-456-104-1
Sequence 1, Application US/08456104
Patent No. 5861310

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.

TITLE OF INVENTION: Tumor Cells Modified to Express B7-2 and B7-3 with Increase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08456,104
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;

APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 107..1093
US-08-456-104-1


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RESULT 3
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 ; Sequence 1, Application US/08479744A
 ; Patent No. 6084067
 ; GENERAL INFORMATION:

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APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-479-744A-1
Query Match 100.0%; Score 1120; DB 5; Length 1120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CACAGGGTGAAGCTTGTCTCTCTCTCTGTACAGGAGCTAGCACAGACACGAT 60
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QY 361 CACAAGTTTATTCGAGCAGTGGACCTGAGACTTCACATCTTCAGATCAAGCA 420
Db 361 CACAAGTTTATTCGAGCAGTGGACCTGAGACTTCACATCTTCAGATCAAGCA 420
QY 421 GGGCTGTATCATATGATCATCCAAACCAAGCAAGATGATGATCCACCA 480
Db 421 GGGCTGTATCATATGATCATCCAAACCAAGCAAGATGATGATCCACCA 480
QY 481 GATGAATTCGAGTGCAGTGTCTGCTAAGACCTCAACCTGAAATAGTACCAATTC 540
Db 481 GATGAATTCGAGTGCAGTGTCTGCTAAGACCTCAACCTGAAATAGTACCAATTC 540
QY 541 TAAATTAACAGAAATGCTATCAATATTTGACCTGCTATCAAGGTTACCCAGA 600
Db 541 TAAATTAACAGAAATGCTATCAATATTTGACCTGCTATCAAGGTTACCCAGA 600
QY 601 ACCTAAGAGATGAGTGTCTGCTAAGACCAAGATTCAGATGATGATGAT 660
Db 601 ACCTAAGAGATGAGTGTCTGCTAAGACCAAGATTCAGATGATGATGAT 660
QY 661 TATGAGAAATCTCAAGATATGTCAGAGAACTGACAGTTCCTCAGCTTGTCTGT 720
Db 661 TATGAGAAATCTCAAGATATGTCAGAGAACTGACAGTTCCTCAGCTTGTCTGT 720
QY 721 TTTATTCCTGATGTTAGAGCAATATGACATCTTCTGATTTCTGGAATGACAAAGAC 780
Db 721 TTTATTCCTGATGTTAGAGCAATATGACATCTTCTGATTTCTGGAATGACAAAGAC 780
QY 781 GGGGTTTATATCTACCTTCTCTATAGAGCTGAGAGCCCTCAGCTCCCAAGCA 840
Db 781 GGGGTTTATATCTACCTTCTCTATAGAGCTGAGAGCCCTCAGCTCCCAAGCA 840
QY 841 CATTCCTGATGTTAGAGCAATATGACATCTTCTGATTTCTGGAATGACAAAGAC 900
Db 841 CATTCCTGATGTTAGAGCAATATGACATCTTCTGATTTCTGGAATGACAAAGAC 900
QY 901 AATTTATGAGAAATGGAAGAAAGAGGCGCTGCACTCTTATATATGTTGAACCA 960
Db 901 AATTTATGAGAAATGGAAGAAAGAGGCGCTGCACTCTTATATATGTTGAACCA 960
QY 961 CACAATGAGAGGAGAGAGAGTGAACAGACCAAGAAAGAGAAATTCATATACCTGA 1020
Db 961 CACAATGAGAGGAGAGAGAGTGAACAGACCAAGAAAGAGAAATTCATATACCTGA 1020
QY 1021 AAGATCTATGAGAGGAGGCTGTTTAAAGTTGCAAGCATCTTCATGACCAAG 1080
Db 1021 AAGATCTATGAGAGGAGGCTGTTTAAAGTTGCAAGCATCTTCATGACCAAG 1080
QY 1081 TGATCATGTTTATTAATTAAGAGTAAAGCCCAAAAAA 1120
Db 1081 TGATCATGTTTATTAATTAAGAGTAAAGCCCAAAAAA 1120

RESULT 4
PCT-US95-02576-22
Sequence 22, Application PC/TUS9502576
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: 65
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandargouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
PCT-US95-02576-22

Query Match 100.0%; Score 1120; DB 6; Length 1120;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACAGGGTGAAGGCTTTGCTCTGCTGCTGTAACAGGAGTACAGACACAGAT 60
Db 1 CACAGGGTGAAGGCTTTGCTCTGCTGCTGTAACAGGAGTACAGACACAGAT 60
QY 61 GAGGGGGTCAATTCAGATATATGATGACAGAGAAAGCCCAATATGATCCAGTG 120
Db 61 GAGGGGGTCAATTCAGATATATGATGACAGAGAAAGCCCAATATGATCCAGTG 120
QY 121 CACATGAGAGTGAATACATCTCTTTGATGAGGCTTCTCTGCTGCTGCTGCTCC 180
Db 121 CACATGAGAGTGAATACATCTCTTTGATGAGGCTTCTCTGCTGCTGCTGCTCC 180
QY 181 TCTGAAGTTCAACTATTTCAATGAGAGTGAAGAGTCCATGCTGCTGCTGCTGCTC 240
Db 181 TCTGAAGTTCAACTATTTCAATGAGAGTGAAGAGTCCATGCTGCTGCTGCTGCTC 240
QY 241 TCAAAACCAAGCCTGAGTGAAGTATTTGGCAGGACGAGAAACTTGTCT 300
Db 241 TCAAAACCAAGCCTGAGTGAAGTATTTGGCAGGACGAGAAACTTGTCT 300
QY 301 GATGAGTATATAGCAAGAAATTTGACAGTTCATTCAGATATGAGCGC 360
Db 301 GATGAGTATATAGCAAGAAATTTGACAGTTCATTCAGATATGAGCGC 360
QY 361 CACAAGTTTATTCGAGCAGTGGACCTGAGACTTCACATCTTCAGATCAAGCA 420
Db 361 CACAAGTTTATTCGAGCAGTGGACCTGAGACTTCACATCTTCAGATCAAGCA 420
QY 421 GGGCTGTATCATATGATCATCCAAACCAAGCAAGATGATGATCCACCA 480
Db 421 GGGCTGTATCATATGATCATCCAAACCAAGCAAGATGATGATCCACCA 480
QY 481 GATGAATTCGAGTGCAGTGTCTGCTAAGACCTCAACCTGAAATAGTACCAATTC 540
Db 481 GATGAATTCGAGTGCAGTGTCTGCTAAGACCTCAACCTGAAATAGTACCAATTC 540
QY 541 TAAATTAACAGAAATGCTATCAATATTTGACCTGCTATCAAGGTTACCCAGA 600

|||||
Db 541 TAAATATACAGAAAATGTGTACATAAATTTGACCTGCATCTATACAGGGTTCCGCA 600
Qy 601 ACCTAAGAAAGATGATGTTTGTCTAGAACCAAGAAATTCACCTATGAGTATGAT 660
Db 601 ACCTAAGAAAGATGATGTTTGTCTAGAACCAAGAAATTCACCTATGAGTATGAT 660
Qy 661 TATGAGAAATCTCAAGATTAATGTCCAGAACTGTACAGCTTTCCATCAGCTTGTCT 720
Db 661 TATGAGAAATCTCAAGATTAATGTCCAGAACTGTACAGCTTTCCATCAGCTTGTCT 720
Qy 721 TTCATTTCCCTGATGTTACAGCAATATGACATCTTCTGTATTTGGAACAGCAAC 780
Db 721 TTCATTTCCCTGATGTTACAGCAATATGACATCTTCTGTATTTGGAACAGCAAC 780
Qy 781 GGGGCTTTATCTTCCATCTTCTGTATGAGCTGTAGAGCCCTGACCTCCCGCAGACCA 840
Db 781 GGGGCTTTATCTTCCATCTTCTGTATGAGCTGTAGAGCCCTGACCTCCCGCAGACCA 840
Qy 841 CATTCCTTGATTAAGCTGTACTTCCAAACATTAATATGTGATGTTTCTGTCT 900
Db 841 CATTCCTTGATTAAGCTGTACTTCCAAACATTAATATGTGATGTTTCTGTCT 900
Qy 901 AATTCATGAAATGGAAGAGAGAGAGCGCCTGCAACTCTTATTAATGTGAAACCA 960
Db 901 AATTCATGAAATGGAAGAGAGAGAGCGCCTGCAACTCTTATTAATGTGAAACCA 960
Qy 961 CACAAATGAG 1020
Db 961 CACAAATGAG 1020
Qy 1021 AAGATCTGATGAAGCCACGCTGTTTAAAGTTGGAAGACATCTTCATGCGACAAAAG 1080
Db 1021 AAGATCTGATGAAGCCACGCTGTTTAAAGTTGGAAGACATCTTCATGCGACAAAAG 1080
Qy 1081 TGATACATGTTTAAATTAAGAGTAAGCCCAAAAAA 1120
Db 1081 TGATACATGTTTAAATTAAGAGTAAGCCCAAAAAA 1120

RESULT 5
PCT-US95-02576-24
; Sequence 24, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BMT-1200PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941

;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1161 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 148..1134
PCT-US95-02576-24

Query Match 90.6%; Score 1014.8; DB 6; Length 1161;
Best Local Similarity 99.8%; Pred. No. 1.8e-287;
Matches 1016; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 103 CAAATGGATGCCAGTCCAGTATGAGAGAGTGAATTCCTCTTTGTGATGACCTTCT 162
Qy 144 CACTATGATCCCGACATGACACTATGAGACTGATACATTTCTTTGTGATGACCTTCT 203
Qy 163 GCTCTGTCGTCCTCTCTCTGGAAGATTCAAGCTTATTTCAATGAGACTGCAAGCTGCC 222
Db 204 GCTCTGTCGTCCTCTCTCTGGAAGATTCAAGCTTATTTCAATGAGACTGCAAGCTGCC 263
Qy 223 ATGCCAATTTCCAAACTCTCAAAACCAAGCTGAGAGCTAGTACTATTTGGGAGGA 282
Db 264 ATGCCAATTTCCAAACTCTCAAAACCAAGCTGAGAGCTAGTACTATTTGGGAGGA 323
Qy 283 CCAGGAAACCTTGTTGATGAGTACTTATGAGCAAGAGAAATTTGACAGTGTCA 342
Db 324 CCAGGAAACCTTGTTGATGAGTACTTATGAGCAAGAGAAATTTGACAGTGTCA 383
Qy 343 TTCCAAGTATATGGGCGCCACAAAGTTTGAATGAGACAGTTGACCTGAGACTTCAAA 402
Db 384 TTCCAAGTATATGGGCGCCACAAAGTTTGAATGAGACAGTTGACCTGAGACTTCAAA 443
Qy 403 TCTTTAGATCAAGGACAAAGGCTGTATCATATGATCATCATCAAAAGGCCACAGG 462
Db 444 TCTTTAGATCAAGGACAAAGGCTGTATCATATGATCATCATCAAAAGGCCACAGG 503
Qy 463 AATGATTCGATCCACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 522
Db 504 AATGATTCGATCCACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
Qy 523 TGAATATGATCCAAATTTCTAATATTAAGAGAAATGTATCAATAAATTTGACCTGTCATC 582
Db 564 TGAATATGATCCAAATTTCTAATATTAAGAGAAATGTATCAATAAATTTGACCTGTCATC 623
Qy 583 TATPACAGCTTACCCAGAACCTTAAGAGATGAGTGTGTTGCTAGAACCAAGAAATTCAC 642
Db 624 TATPACAGCTTACCCAGAACCTTAAGAGATGAGTGTGTTGCTAGAACCAAGAAATTCAC 683
Qy 643 TATPACAGCTTACCCAGAACCTTAAGAGATGAGTGTGTTGCTAGAACCAAGAGCTGACAGCT 702
Db 684 TATPACAGCTTACCCAGAACCTTAAGAGATGAGTGTGTTGCTAGAACCAAGAGCTGACAGCT 743
Qy 703 TTCCATCAGCTTGTCTGTTTCAATCCCTGATGTTACGAGCAATATGACCAATCTTGTAT 762
Db 744 TTCCATCAGCTTGTCTGTTTCAATCCCTGATGTTACGAGCAATATGACCAATCTTGTAT 803
Qy 763 TCTGGAACCTGACAGAGAGCGGCTTTATATCTTACCTTCTCTATATGAGCTTACAGAGCC 822
Db 804 TCTGGAACCTGACAGAGAGCGGCTTTATATCTTACCTTCTCTATATGAGCTTACAGAGCC 863
Qy 823 TCAGCTCCCGCAGACCAATTCCTGATGATGATGATGATGATGATGATGATGATGATG 882
Db 864 TCAGCTCCCGCAGACCAATTCCTGATGATGATGATGATGATGATGATGATGATGATG 923
Qy 883 TGTGATGTTTCTGTCTAATTTATGAAATGGAAGAAAGAGAGAGAGAGAGAGAGAGAG 942
Db 924 TGTGATGTTTCTGTCTAATTTATGAAATGGAAGAAAGAGAGAGAGAGAGAGAGAGAG 983

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGGGTGAAGCTGCTTCCTGCTGCTGAACAGGAGGACAGACAGACAGGAT 60

Db 1 CACAGGGTGAAGCTGCTTCCTGCTGCTGAACAGGAGGACAGACAGACAGGAT 60

QY 61 GAGTGGGTCATTTCGATATATAGTACAGCAGAAACCAAAATGGATCCCGAGTG 120

Db 61 GAGTGGGTCATTTCGATATATAGTACAGCAGAAACCAAAATGGATCCCGAGTG 120

QY 121 CACT 124

Db 121 CACT 124

RESULT 15
PCT-US95-02576-41
; Sequence 41, Application PC/TUS9502576

; GENERAL INFORMATION:

; APPLICANT: TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules

; TITLE OF INVENTION: and Uses Therefor

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/02576

; FILING DATE: PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/205,697

; FILING DATE: 02-Mar-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 41:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 195 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; FEATURE: MOLECULE TYPE: CDNA

; NAME/KEY: CDS

; LOCATION: 148..195

; PCT-US95-02576-41

Query Match 4.7%; Score 53; DB 6; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 GCACTATGGGACATGATACATCTCTTGTGATGGCCTTCCTCTCTGTG 172

Db 143 GCACTATGGGACATGATACATCTCTTGTGATGGCCTTCCTCTCTGTG 195

Search completed: November 6, 2000, 00:41:05
Job time: 31234 sec

PA (DAND) DANA FARBER CANCER INST INC.
 PA (REP) REPLIGEN CORP.
 XX Freeman GJ, Gray GS, Nadler LM;
 XX WPI: 1997-077269/07.
 DR P-PSDB: W08467.
 XX
 PT DNA encoding a B7-2 fusion protein - used to enhance or down
 FT regulate B lymphocyte antigens
 XX
 PS
 XX Example 4: Page 93-94; 171pp: English.
 CC A cDNA clone (T49181), designated clone 29, codes for the
 CC B-lymphocyte antigen B7-2 (W08467), a CTLA4/CD28 ligand which
 CC costimulates T cell activation. It was obtd. by transfecting COS
 CC cells with a human anti-igm activated B cell cDNA library, reacting
 CC transfectants with CTLA4ig and CD28ig, and panning with anti-human
 CC IgG antibody. E. coli transfected with a vector contg. the cDNA
 CC insert of clone 29 was deposited as ATCC 69357. Nucleic acids
 CC encoding the extracellular domain, variable region-like domain or
 CC constant region-like domain of B7-2 (see also T49197-98) are used
 CC to construct novel fusion proteins with e.g. an immunoglobulin
 CC constant region. These can be expressed in host cells and used to
 CC enhance or suppress T cell-mediated immune responses.
 CC
 XX
 SQ Sequence 1120 BP: 354 A; 237 C; 230 G; 299 T; 0 other;

Query Match 100.0%; Score 1120; DB 18; Length 1120;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGGGTAAAGCTTGTCTGCTGCGCTGTACAGGAGTACAGACAGACAGGAT 60
 |||||||
 Db 1 cacagggtaaaagcttgccttcctcgcgcgtacagaggactacacagacagagat 60
 QY 61 GAGTGGGGTCATTTCCAGATTTAGTGCACAGAGACGCCAAATGGATCCCAGTG 120
 |||||||
 Db 61 gagtggggcattccagatattagtgccacagagaagacaaaatggatccccagtg 120
 QY 121 CACTATGGAGCTGAGTAAACATTTCTTTGTGATGGCTTCTGCTGCTGCTGCTGC 180
 |||||||
 Db 121 caactatggagctgagtaaacattctcttgtagtgccttcgcgcctcgcgcctc 180
 QY 181 TCTGAAGATTCAAGCTTATTTCATGAGAGCTGAGACCTGCCATGCCATTTGCAAACTC 240
 |||||||
 Db 181 tctgaagattcaagcttatttcataagagactgcagaccctgcacattgcacaacc 240
 QY 241 TCAAAACCAAGCGCTGAGTACAGTATGTTTGGCAGAGCAGAGAAACTGGTTCT 300
 |||||||
 Db 241 tcaaaaccaagcctgagtagtagtatttggcagagcaggaactggttct 300
 QY 301 GAATGAGTATTAAGGCAAGAAATTTGACAGTGTTCATTCAGATATATGGCGG 360
 |||||||
 Db 301 gaatgagtataacttagcaagaagaattgcagtgctcattccaaatlataatggcg 360
 QY 361 CACAAGTTTGAATGGAGAGCTGAGACCTGAGACCTTCAATCTCAGATCAAGACAA 420
 |||||||
 Db 361 cacaagtttgaatggagagctgagaccctgagacttcaaatcttcagatcaagaaca 420
 QY 421 GGGCTTGATCAATGATCATCCATCACAATAAGGCCACAGAAATGATTGCAATCCAGCA 480
 |||||||
 Db 421 gggcttgatcaatgatcatccatcacaataaggccacagaatgattgcattccagca 480
 QY 481 GATGAATTCTGAACGTGCTGCTGCTTAATCTTCACTCAACCTGGAATAGTACCATTTC 540
 |||||||
 Db 481 gatgaattctgaacgtgctgctgcttaattcttcaactcagaccggaatagttaccatttc 540
 QY 541 TAATATAAGAAATGTGATCAATTAATTTGACCTGCTCATATACAGGTTACCAGCA 600
 |||||||
 Db 541 taataataagaaatgtgatcaatataatTTGACCTGCTCATATACAGGTTaccagca 600

QY 601 ACCTAAGAAGATGATGCTTTTGGTAAAGCAAGAAATTCAGTATGAGTATGATGAT 660
 |||||||
 Db 601 acctaagaagatgattgttttgcctaagaaccaagaattcaactatcagatcagatgatt 660
 QY 661 TATGCAAAATCTCAAGATTAATGTACAGAACTGTACAGAGTTTCCATAGCTTGTCTGT 720
 |||||||
 Db 661 tatgcaaaatctcaagattaatgtacagaaactgtacagagtttccatagctgtctgtc 720
 QY 721 TTGATTCCTTGATGTTAGCAGCAATATGACCATCTTCTGTATTTCTGAAACTGACAAAC 780
 |||||||
 Db 721 ttgatctcttgatgtttagcagcaaatatgaccatcttctgtattcttgaaactgacaagac 780
 QY 781 GCGGCTTTTATCTTACACCTTTCTCTATAGAGCTTTGAGAGCCCTGACGCTCCCAAGACCA 840
 |||||||
 Db 781 gcggttttatacttccacttctctataagagcttgagaccctcagctccccaagacca 840
 QY 841 CATTCCTTGATTTACAGCTGATCTTCCAAACAGTATTAATGATGATGATGTTTCTGTCT 900
 |||||||
 Db 841 catctcttgatttacagctgatttccaaacagttatataatgtagtggtgttctgtct 900
 QY 901 AATTCTATGGAATGGAAGAAGAAAGCGCTCGCACTTTATTAATGTGAAACCAA 960
 |||||||
 Db 901 aattctatggaatggagaagaagaagcgctcgcgaactcttataatgtgaaaccaa 960
 QY 961 CACAATGAGAGGAGAGAGAGTGAACGACCAAGAAAGAAATCCATATACCTGA 1020
 |||||||
 Db 961 cacaatgagagagagagagtgacacagcaagaagaagaataatccatatacctga 1020
 QY 1021 AAGATCTGATGAGCCCGAGCTGTTTAAAGTTTCAAGACATCTTCATGCGACAAAG 1080
 |||||||
 Db 1021 aagatctgatgagcccgagctgtttttaaagtttcaagacttctcatcagcgacaaag 1080
 QY 1081 TGATACATGTTTAAATTAAGAGTAAAGCCCAAAAAA 1120
 |||||||
 Db 1081 tgatacatgttttaattaaagagtaagcccaaaaaa 1120

RESULT 3
 V55784 ID V55784 standard; cDNA; 1120 BP.
 XX

V55784: 23-MAR-1999 (first entry)
 XX

Human B7-2 antigen coding sequence.
 DE

B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
 CTLA4 ligand; therapy; T-cell response; human; ss.
 KW

Homo sapiens.
 OS

Key Location/Qualifiers
 FH 107..1096
 FT CDS /tag= a
 FT

US5861310-A.
 PN

19-JAN-1999.
 PD

30-MAY-1995; 95US-0456104.
 PF

30-MAY-1995; 95US-0456104.
 PR

03-NOV-1993; 93US-0147773.
 PR

(DAND) DANA FARBER CANCER INST INC.
 PA

Freeman GJ, Gray GS, Nadler LM;
 PI

WPI: 1999-130394/11.
 DR

P-PSDB; W73638.
 DR

Tumour cell transfected to express B7-2 molecule - useful for tumour
 PT


```

1
QY 120 GCATATGGAGTAGTACATTCCTTTGATGAGCCTTCCTGCTCTCTGCTGCTC 179
DB 147 gcatataggagctagagtaacattctcttctgtagggctctctctctgctgctc 206
QY 180 CTCTGAAGATTCAGACTTATTTCAATGAGACTGCAGACCTGCATGCCAATTTGCAAACT 239
DB 207 ctctgaagattcaagcttattctcaatgagactgcagacctgcacatgccaatttgaact 266
QY 240 CTCAAAACCAAGCCTGAGTACAGTACATGATATTTTGGCAGAGCAGCAAACTTGCTTC 299
DB 267 ctcaaaccaagaccctgagtagcttagatatttggcagagcacaagaaaacttggctc 326
QY 300 TGAATGAGTACTTGTGCGCAAGAAATTTGACAGTGTTCATCTCCAAATATATAGGCGC 359
DB 327 tgaatgagtactacttggcacaagaatttgacagtggttccattccaaagtatatggc 386
QY 360 GCACAAGTTTGAATCGACAGTTGACCCCTGAGACTTCACAACTTTCAGATCAAGACA 419
DB 387 gcacaagtttgaatcgcagacttgaccctgagacctgagacttcaatctcagatcaagaca 446
QY 420 AGGCTGTGATCATGATCATCATCAAAAAGCCACAGCAATGATTTGGCATCCACC 479
DB 447 aggctctgtatcaatgatacctccacaaaagccacaggaatgtatcgcacacc 506
QY 480 AGATGAATTCGAATGCTGAGTCTGCTTAATTCAGTCAACTGAAATAGTACCAATTT 539
DB 507 agatgaattctgaactctcagctcagtgctgtctaacttcagtcacacctgaaatgtaccaatt 566
QY 540 CTATATTAACAGAAAATGTGTACATAAATTTGACCTGCTCATATACAGGTTACCCAG 599
DB 567 ctataataacagaaaatgtgtacataaattgacctgtccatcatcacaggttaccag 626
QY 600 AACCTAAGAAGATGATGTTTGTGTAAGAACCAAGAAATTCACATGAGAGATATGTTA 659
DB 627 aacctaagaagatgagtggttctgtaagaacaaagaaattcaacatcagatcagatggtla 686
QY 660 TTATGCAAAATCTCAAGATTAATGTACAGAACTGTACAGAGTTTCATCAGCTTGTCTG 719
DB 687 ttatgcagaatctcaagataatgtcacagactgtacagactgttccatcagcttgcctg 746
QY 720 TTTTCATCCCTGATNGTACAGAGCAATATGACATCTTCTGTATTTCTGGAACCTACAGA 779
DB 747 ttccatccctgagttacagagaataatgaccatcttctgtatcttgyaaactgacaga 806
QY 780 CGCGGCTTTATCTTACCTTCTCTATAGAGCTTGAAGACCTCCAGCCTCCCCAGACC 839
DB 807 cgcggctttatcttctcccttctctatagagcttgagaccctccagccctccccaagacc 866
QY 840 ACATTCCTTGAGATTACAGCTGTACTTCCAAAGTTATATATGTGTATGGTTTCTGTC 899
DB 867 acattccttgatcaagctgtacttccacaagttatataatgtatgtgtttctgctc 926
QY 900 TAATTCATGGAATAAGAAAGAAAGAGGCGCTCCCAACTCTTATTAATGTGGAACCA 959
DB 927 taattctatggaatggaagaagaagaagcgctcgaactcttataaaltgtyaacca 986
QY 960 ACACAATGAGAGGAGAGAGAGTGAACAGACCAAGAAAGAAAGAAATCCATTTACTCTG 1029
DB 987 acacaatgagagaggaagagagtgaaacagaccaaagaagaagaaaaatccatatctctg 1046
QY 1020 AAAGATCTGATGAAGCCAGCGTGTTTTAAAGTTGGAAGACATCTTTCGACAAAA 1079
DB 1047 aaagatctgtagaagccagcggtttttaaagttcgaagacatcttcatgacaaaa 1106
QY 1080 GTGATCATGTTTATTAATTAAGGTAAGCCCAAAAA 1118
DB 1107 gtgatacatggtttttaaataaagaagtaagccatacaa 1145

```

RESULT 6
V83208
ID V83208 standard: cDNA: 972 BP.
XX

```

AC V83208:
XX 02-MAR-1999 (first entry)
DT B7-2 cDNA.
XX Mouse: immunodeficient; pathogen: tumour; lymphocyte: antigen;
KW immunomodulator; vector: vaccine; cancer: HIV; leishmania;
KW Mycobacterium; listeria; plasmidium; retrovirus; evaluation;
KW human immunodeficiency virus; ds.
OS Homo sapiens.
XX
XX M09844788-A2.
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98WO-US06944.
XX
XX 09-DEC-1997; 97US-0069163.
XX 09-APR-1997; 97US-0838702.
XX 01-MAY-1997; 97US-0848760.
XX
XX (CHAN/) CHANG L.
XX
XX Chang L;
XX WPI: 1999-024005/02.
XX
XX Use of immunodeficient mice comprising human cells - particularly
PT SCID/Beige mice comprising human immune cells for evaluating
PT vaccines against cancers or human pathogens, e.g. HIV
XX
XX Example 1b: Page 104-105; 154pp; English.
XX
XX Immunodeficient mice comprising human cells can be used for
XX exposure to human pathogens and/or their components or human
XX tumour cells and human peripheral blood lymphocytes. Also claimed
XX is a vaccine comprising a cell modified to express an antigen and
XX an immune-modulating protein, this is preferably an expression
XX vector comprising a polynucleotide sequence that encodes the
XX antigen and immune-modulating protein. Such vectors can be used
XX to treat a subject having a tumour by transferring the expression
XX vector into the tumour so that the antigen and the immune-modulator
XX are expressed by at least the tumour. The methods can be used for
XX producing and evaluating vaccines including cancer vaccines and
XX vaccines directed against human pathogens, e.g. HIV, leishmania,
XX Mycobacterium, listeria or plasmidium. This sequence is an
XX intermediate retroviral vector derived from pLNL6, a vector approved
XX for clinical use in the United States. pLNL6 is essentially pLNL6
XX digested with ClaI and BclI to remove cloning sites and the pLNL6
XX internal Sneo gene. These were replaced with a polylinker. A neo
XX gene was then inserted under the transcriptional control of the SV40
XX enhancer/promoter to create the vector pLSN. Two primers (V83187,
XX CC CD28/CTLA-4 proteins, co-stimulators for interleukin-2 driven
XX proliferation of T-cells) for its insertion into pLSN.
XX
XX Sequence 972 BP: 304 A; 204 C; 194 G; 270 T; 0 other;
XX
Query Match 86.8%; Score 972; DB 20; Length 972;
Best Local Similarity 100.0%; Pred. No. 1.9e-281;
Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 ATGGAGCTGAGTAACATTCCTTTGATGAGCCTTCCTGCTCTCTGCTGCTC 184
DB 1 atggagctgagtaacattctcttctgtagggctctctctctgctgctcctcctc 60
QY 185 AAGATTCAAGCTTATTTCAATGAGACTGCAGACCTGCCAATTTGCAAACTGCA 244
DB 61 aagattcaagcttattctcaatgagactgcagacctgcacatgccaatttgaactcaa 120

```



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QY 245 AACCAAGCCTGAGTACGCTAGTATATTTGGCAGACACAGAAAAGCTGGTTCGAAT 304
    |||
Db 121 aaccaaagcctgagtgagctagtagtatttggcagagcaccagaaacttgcttgat 180
QY 305 GAGGTATCTTATGCAAGAAAGAAATTTGACAGTGTTCATTCGAATATATGGCCGAC 364
    |||
Db 181 gaggtatctttagcaagaagaatttgcagtgcttccaaagtataatggccgcaca 240
QY 365 AGTTTGTGATGGAGAGTGGAGCCCGGAGACTTCACAAATCTTCAGATCAAGGACG 424
    |||
Db 241 agtttgcatttcggaagcttgagacctgagatcccaatcttcagatcaagaagggc 300
QY 425 TTGTATCAATGTATCATTCATCACAAGAACCCACAGAGATGTCGATCCACAGATG 484
    |||
Db 301 ttgtatcaatgtatcatctcatcaaaaagccacagagatgattcgcataccagatg 360
QY 485 AATTCGAACCTGTCAGTGTCTGCTAATCTCAGTCACAACTGAATGTACCAATTTCTAT 544
    |||
Db 361 aattcgaactgcaagtgcttctaacttcaaccctgaaataagtaacaaatlctcaat 420
QY 545 ATACAGAAAATGTGTACATTAATTTGACCTGCTCATCTATACAGGTTACCCAGAACCT 604
    |||
Db 421 atacagaaaatgtgtacataaaattgacctgtcatctatacaggttacccagaaact 480
QY 605 AGAGAGATGAGTGTGTTGCTAAGAACCAAGAAATTAAGTATGATGATGATATG 664
    |||
Db 481 aagaagatgagtgcttctgaagaacaaagattcaacatacgatgatgtatatacg 540
QY 665 CAGAAATCTCAATATATGTCACAGAACTGACGAGTTCCATCAGCTTGCTGTTTCA 724
    |||
Db 541 cagaatactcaagataatgtcacagaaactgtacagacgttccacagcttgctgttca 600
QY 725 TTCCTGTGATGTACGACATATATGACCATCTCTGTATTCGGAACCTGACAGACGG 784
    |||
Db 601 ttccctgattgtacgagcaatagacacatctctgtatcttgaactgcaagacgag 660
QY 785 CTTTATCTTCACCTTCTCTATAGAGCTTGAGAGCCCTAGGCTCCCGACACCAAT 844
    |||
Db 661 ctltatcttcacacttctctatagagcttgaggaacctcagacctcccaagacaat 720
QY 845 CCTGTGATGTACGCTGACTTCCAACTGATATATATGATGATGATGATGATGAT 904
    |||
Db 721 cctgtgattcaagctgacttcaaccagatataatagtgatgtgttctcttcaat 780
QY 905 CTATGAATGTGAAGAAAGAACGGCGCTGCAACTCTTATAAATGTGAACCAACACA 964
    |||
Db 781 ctatgaaatggaagaagaagcgcctcgcacacttataaattggaacacaaca 840
QY 965 ATGAGAGAGGAGAGAGTGAACACAGACCAAGAAAAGAAAATCCATATACCGAAGA 1024
    |||
Db 841 atggaagagggaagagatgacacagcaagaagaagaataacccatataccctgaaaga 900
QY 1025 TCTGATGAGCCGACGCTGTTTAAAAAGTTCGAAAGACATCTTCATCGACAAAAGTAT 1084
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Db 901 tctgatgagcccgctggttcttcaaaaagtcgaagaatcttcacgcaaaaagtgat 960
QY 1085 ACATGCTTTTAA 1096
    |||
Db 961 acatgtttttaa 972

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KW human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 52..126
FT /*tag= a
FT mat_peptide 127..831
FT /*tag= b
XX
PN MO9747732-A2.
XX
PD 18-DEC-1997.
XX
PE 13-JUN-1997; 97WO-0512599.
XX
PR 21-FEB-1997; 97US-0038915.
PR 14-JUN-1996; 96US-0019934.
PR 19-FEB-1997; 97US-0043948.
XX
PA (SMK ) SMITHKLINE BEECHAM CORP.
XX
PI Chalklin MA, Lyn SDP, Sweet RM, Truneh A;
XX
DR WPI: 1998-052299/05.
XX
P-PSDB: W32339.
XX
PT Hexameric fusion protein containing IgA antibody fragment - used for
PS stimulating CD28 positive cells, or suppressing CTLA-4 positive
XX cells
XX
PS Example 1; Fig 5A-B; 105pp; English.
XX
XX
CC This DNA sequence comprises a portion of plasmid CD86calphatplink
CC that codes for the signal region and extracellular domain (see
CC W42339) of human CD86 extracellular domain. The plasmid encodes a
CC fusion protein comprising the CD86 signal peptide and extracellular
CC domain grafted to a human IgG1 heavy chain Fc region and the
CC tailpiece region (alpha-tp) (see W42344) of human IgA heavy chain.
CC The processed fusion protein has been expressed as a hexamer in COS
CC cells. The invention relates to novel hexameric fusion proteins
CC comprising a dimeric binding protein such as CD86 provided at its
CC C-terminus with a tailpiece that has the activity of alpha-tp. The
CC tailpiece provides the fusion protein with the ability to form
CC stable hexamers. Also claimed are polynucleotides encoding the
CC hexameric fusion proteins, vectors, recombinant host cells and a
CC method for producing the hexamers. The fusion protein is useful in
CC therapeutics and vaccines, and is particularly well suited for
CC applications for which the binding protein from which it is derived
CC is unsatisfactory because of low binding affinity or for
CC applications where multivalency is desired. Applications include
CC diagnostics, binding assays and screening assays. CD86-Ig-alpha-tp
CC fusion protein is used in claimed methods for stimulating CD28
CC positive cells or suppressing CTLA-4 positive cells.
XX
SO Sequence 831 BP; 247 A; 201 C; 162 G; 221 T; 0 other;

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Query Match 67.2%; Score 753.2; DB 19; Length 831;
Best Local Similarity 99.0%; Pred. No. 6; Se-216;
Matches 758; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 81 ATTAGTCAACGAGAGAGAGCAAGCAAAATGAGTCCCGAGTGCATATGAGAGTGAACA 140
    |||
Db 26 attcgtacacagcagagaagcagcaaaatgatactcccgagtcactatgagactgaaca 85
QY 141 TTCTCTTTGATGAGGCTTCTCTGCTCTCTGTGCTGCTCTCTGAGAGATTCAAGCTATT 200
    |||
Db 86 ttctcttggatggccttcctctctctctgtctgtctgtcctcgaagattcaagcttact 145
QY 201 TCAATGAGAGTGGAGAGACTGCGCATGCCAATTTGCAAACTCTCAAAACCAAGCGTGA 260
    |||
Db 146 tcaagagacugcagacctgcacatgtccaatttgcacaactcacaacaaagcctgagtg 205

```

RESULT 7
 V03230 standard; cDNA; 831 BP.
 V03230:
 22-JUN-1998 (first entry)
 DNA encoding CD86 extracellular domain in CD86calphatplink.
 Hexameric fusion protein; IgA; alpha-tp; tailpiece; antibody;
 CD86; CD28; CTLA-4; vaccine; diagnosis; binding assay; screening;


```

Db      481  |||||
         aagaagagagcgtcttcgctaagaaccaagaatcgaactatcgatgatggtattatg 540
QY      665  CAGAAATCTCAAGTAATATGTCACAGAACTGTACGAGCGTTTCCATCAGCTTGTCTGTTTCA 724
Db      541  cagaatctcgaagtaatgctacagaactgtaagcagcttccatcagactgctgcttca 600
QY      725  TTCCCTGATGTTTAGAGCAATATGACATCTTTCGTATTCGTGGAACTGACAGACGCG 784
Db      601  ttccctgctgtaagagaatataagacactcttcgctatctcgaactcgaaagaagcg 660
QY      785  CTTTATATCTTCACTTCCTCTATAGAGCTTGAGGACCTCAGCCTCCGCCAGACCAT 844
Db      661  ctttatcttcaacttctctcatagagcttgaggacctcactcccccagaccacatt 720
QY      845  CCTTG 849
Db      721  cctgg 725

RESULT 9
ID      227913 standard; DNA; 1897 BP.
XX      227913;
AC      227913;
XX      20-DEC-1999 (first entry)
DT
DE
XX      Canine B7-2 protein encoding DNA.
XX
XX      B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX      allergic reaction; infectious disease; tumor development; canine;
XX      graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX      Canis familiaris.
XX
XX      W09947558-A2.
XX      23-SEP-1999.
XX
XX      19-MAR-1999; 99WO-US06187.
XX
XX      19-MAR-1998; 98US-0078765.
XX      17-APR-1998; 98US-0062597.
XX
XX      (HESK-) HESKA CORP.
XX
XX      Sim G, Yang S, Sellins KS.
XX      WPI; 1999-571822/48.
XX      DR      P-PSDB; Y41076.
XX
XX      New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX      treating, e.g. autoimmune and atopic diseases
XX
XX      Claim 1; Page 97-99; 148bp; English.
XX
XX      The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX      encoding nucleic acid molecules from dogs and cats. The proteins can be
XX      expressed by standard recombinant methodology. The nucleic acid molecules
XX      and the encoded proteins can be used for preventing or treating diseases,
XX      e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX      development, graft rejection, inflammatory, arthritic and atopic diseases
XX      such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX      cats, cattle, sheep or pets. The products can also be used for detection,
XX      diagnosis and drug screening.
XX
XX      Sequence 1897 BP; 585 A; 400 C; 383 G; 529 T; 0 other;
XX
Query Match 53.3%; Score 597; DB 20; Length 1897;
Best Local Similarity 78.2%; Pred. No. 6, 4e-169;
Matches 798; Conservative 0; Mismatches 205; Indels 18; Gaps 6

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Oy	102	CCAAATATGATCCCACTGTCATATGGACATGAGTAACATATCTCTTTGATAGGCCCTTCG	161
Db	1	ccaagaatgtaattcccaatgtaactatgtaactatgaaactatcaatctctcttgtaagacccttc	60
Oy	162	TGCTCTCTGGGAGCGCTCCCTGTAATGATTCAGATTCAGATCTTATTTGAATGAGACATGCGAGACTGC	221
Db	61	tgctctatggtgtgtcttccatcagaagaagcaagcattcttcaacaagaagcggaagctcg	120
Oy	222	CATGCCAATTTTGCAAACTCTCAAAACCAAAAGCTTGATGAGCTAGTATTTTGGCAGG	281
Db	121	catgcattttacaattcccaataaataagccttgaaatgtaagttgtaagttcttggaag	180
Oy	282	ACCGAGAAACTTGGTCTCTGAATGAGCTATCTTGGCAAGAGCAAAATTTGACAGTGTCT	341
Db	181	accaggaataagcttggtctgtacagactatcacagaagagcaagaagaccctcacaatgctc	240
Oy	342	ATTCACAGTATATGGGCGCGACAAAGTTTTGATTTGGAGAGTTGGACCCCTGAGACTTCACA	401
Db	241	atcgcaagtataaaggcgccgacaagcttttgacaagaacaaatgagcccttgagctccata	300
Oy	402	ATCTTCAGATCAGAGACAGAGGCGTTGTATCAATGTATCATCATCACAAAAAGCCACAG	461
Db	301	atatccagatlaaagagaacaagggctgtatcaatglttgcattcatataaaggcgccaag	360
Oy	462	GAATATTCGGATCCAGCACAGATGAATTTCTGAACTGTCAGATGCTTGCTCAACTTCAGTCAAC	521
Db	361	gactcgtctccatgacacagagaatattctgacctaaatcgtgttgcataacttcagtaac	420
Oy	522	CTGAATATGATACCAATTTGTAATATACAGAAAA--TGTGTACATAAATTTGACCTGCT	578
Db	421	ctgaataatgtaacttcaactctatagaacaagaatattctgtgcataataatttgaccgtc	480
Oy	579	CATCATATCAGCGTTTACCCAGAACCTTAAGAAATGATGATGTTTGGTAGAACCAAGATTT	638
Db	481	catccaataaagggttacccagaaacccaagagagatgatttcttgtaaaaaccgagaatt	540
Oy	639	CAACTATGAGATGATGATGATTTATGACAAATCTCAGATATATGTCCACAGACTGTAACG	698
Db	541	caagtaactaagtaatactatgtaactgtcatgagaatactcaaatatgtaacagaactca	600
Oy	699	ACGTTTCATCAGCTGTGCTGTTCATCTCCGTATGATGTAAGAGCAATPTAGCAATCTCT	758
Db	601	acgtttctatcaagctgttgccttccacagctcccgaa--caagcaatgtgagcattctct	657
Oy	759	GATATCTCGAAACTGACAAAGCGGGCTTTTATCTTACACTTCTCTATAGA--GCTTG	815
Db	658	ggtctcgtgaactatgagtaactgaagcttccctccactataataatgtaagtaata	717
Oy	816	AGGACCTCAGCCTCCCCAGACACACATTTCTTGATTTACAGCTGTACTTCCAA---CAG	872
Db	718	cgaaaccacccctatgaaagacacacactcctcgtatgtcggtctgcttgaatgttg	777
Oy	873	TATATATATGATGATGATGTTTCTGTCTTAATTTCAATGAGAAATGGAAGAAAGAGCGGC	932
Db	778	tcaatttgtgtgagtggtgtcttcttcaactaaaggaaa---aggaagaagaagcagc	834
Oy	933	CTTCGCAACTCTTATTAATGTGGAACAACAACATGAGAGGAGAGAGACTGAACGACCA	992
Db	835	cttgcgccctcatgaatcgtgaaacacaagaagtgaggaanaagaaatgtgacagacca	894
Oy	993	AGAAAAAGAAAAAATTCGATTAATCTCAAAAGATCTGATGTAAGGCCGAGCTGTTTTAAAA	1052
Db	895	aggaagaagtaagtaaccatagaagaagaataccctgtatgaagcccggtgt---ttaaca	951
Oy	1053	GTTTCGAGAGCATCTTCATGCGACAAAAGTGATGATGTTTATTAATTAAGAGTAAGGCC	1112
Db	952	tttcgagaagcagcttcagcgcgacaacagtaactacacagtttlaataaagagtaaaagtc	1011
Oy	1113	A 1113	
Db	1012	a 1012	

us-09-206-132-1.rng

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2000, 04:34:36 ; Search time 818.59 Seconds
(without alignments)
8459.355 Million cell updates/sec

Title: US-09-206-132-1
Perfect score: 1120
Sequence: 1 CACAGGGTGAAGCTTGCT.....AGAGTAAAGCCCAAAAAA 1120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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QY 1075 CAAAGTACATGTTTAAATTAAAGTAAGCCCAAAAA 1118
|||||
Db 361 CAAAGTATACATGTTTAAATTAAAGTAAGCCCATACAA 404

RESULT 2
AA056906 448 bp mRNA EST 18-SEP-1996
LOCUS EST224R Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)
DEFINITION Sus scrofa cDNA clone SPL224 reverse similar to L25259 CTLA4
counter-receptor, human, mRNA sequence.

ACCESSION AA056906
VERSION AA056906.1 GI:1549546
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 448)
AUTHORS Tuglie,C.R., Wahls,S. and Schmitz,C.
TITLE Expressed Sequence Tags from Pig Spleen
JOURNAL Unpublished (1996)
COMMENT Contact: Tuglie CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ctuglie@iastate.edu

PCR Primers
FORWARD: TGCGCAGCAGCTCCTG
BACKWARD: GACCGGCGCTCAGCT
Insert Length: 950 Std Error: 50.00
Seq primer: GACCGGCGCTCAGCT.

FEATURES
Location/Qualifiers
source 1..448
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="SPL224"
/clone_lib="Pig Spleen lambda gt 11 Library (Clontech Cat
PL1006b)"
/issue_type="spleen"
/dev_stage="adult"
/note="Oligo (dt) primed"

BASE COUNT 126 a 116 c 89 g 116 t 1 others
ORIGIN

Query Match 26.8%; Score 299.6; DB 1: Length 448;
Best Local Similarity 80.8%; Pred. No. 4.5e-75;
Matches 361; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 143 CTCTTTGTGATGGCCCTTCGCTCTGTCGTCG-CTCCTGGAAGATTCAAGCTTATTT 201
|||||
Db 1 CTCGTTGGAGGTCCTCCGCTGCTGTCGTCCTCTGNAAGATCAGGCATATTT 60

QY 202 CAATGAGACTGCAGACCTGCATCCCAATTGCAAACTCCAAACCAAGCCCGATGA 261
|||||
Db 61 CAATGAGACTGCAGACCTGCATCCCAATTGCAAACTGCAGAACCTTAAGCTGATGA 120

QY 262 GCTAGTATATTTGGCGAGCAGGAAGAACTGTTCTGAATGAGTATCTTAAAGCAA 321
|||||
Db 121 GCTGTCATATTTGGCGAGCAGGATACCTGTTCTCAGACGCTATTCGAGGCCA 180

QY 322 AGAGAAATTTGACAGTTCATTCAGATATATGGCCGACAAAGTTTGAATTTGGACAG 381
|||||
Db 181 AGAGAAAGCTCATATATGTTAATTCAGATATGCGTGCACAAAGCTTTGACCGACAC 240

QY 382 TTGGACCTGAGACTTCACATCTTCAGATCAAGGAGGCTTGTATCAATGATATCAT 441
|||||
Db 241 CTGGACCTGAGACTTCACAGCTTCATCAAGGAGGCTTGTATCAATGATATCAT 300

QY 442 CCATCAGAAAAAGCCACAGGAATGATTGCGATCCACCAGATGAATTCTGAAGTGTCACT 501

Db 301 CCATCAATAAAGGCGCATGACTGTGCTATCCACACAGATAGTGTGACTATACAGT 360
|||||

QY 502 GCTTGCTAACTTCACTGACCTGGAATAGTACCAATTTCTAATATACAGAAATGTGA 561
|||||

Db 361 GCTTGCTAACTTCACTGACCTGGAATAGTACCAATTTCTAATATACAGAAATGTGTG 420

QY 562 CATAAATTTGACCTGCTCATCTATACA 588
|||||

Db 421 CATAAATTTGACCTGCTCATCTATACA 447

RESULT 3
A1093604/c 570 bp mRNA EST 10-NOV-1998
LOCUS ou82B09.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1634297 3 similar to SW:CD86_HUMAN P42081 T LYMPHOCTYE
ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.

ACCESSION A1093604
VERSION A1093604.1 GI:3432580
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 801 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 400.

FEATURES
Location/Qualifiers
source 1..570
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1634297"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NbhsF pool 1:
309384-310919, 323208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-153327 Soares Nb2HR-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326653 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 107 c 134 g 173 t
ORIGIN

Query Match 23.1%; Score 258.4; DB 8: Length 570;
Best Local Similarity 92.8%; Pred. No. 3.2e-63;
Matches 282; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 815 GAGGACCTCAGCCTCCCGACAGACACATTCCTTGATTAACAGCTTACTCCACAGATT 874
|||||

Db 570 GAGGACCTCAGCCTCCCGACAGACACATTCCTTGATTAACAGCTTACTCCACAGATT 511

[illegible]

```
OY 1034 GCCCAGCGTGTCTTAAAGTTCGAGACATCTTCATCGACAAAGTGATCATGTCTT 1093
DB 124 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 65
OY 1094 TAATTAAAGAGTAAGCCCAAAAAA 1119
DB 64 AATWTATAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 39
```

Search completed: November 5, 2000, 16:41:51
Job time: 43635 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 6, 2000, 01:12:43 ; Search time 360.87 Seconds
(without alignments)
29,126 Million cell updates/sec

Title: US-09-206-132-2

Perfect score: 1733
Sequence: 1 MDPQCTMGSLNLFVMAFL.....AQRVFKSKTSCKDSKDTCE 329

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt-39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	100.0	329	1	CD86_HUMAN
2	963.5	55.6	330	1	CD86_RABIT
3	743.5	42.9	309	1	CD86_MOUSE
4	244	14.1	306	1	CD80_MOUSE
5	243	14.0	299	1	CD80_RABIT
6	201.5	11.6	288	1	CD80_HUMAN
7	179	10.3	524	1	BUTY_MOUSE
8	167	9.6	526	1	BUTY_HUMAN
9	165.5	9.5	558	1	Y653_HUMAN
10	162	9.3	526	1	BUTY_BOVIN
11	128	7.4	274	1	OX2G_HUMAN
12	128	7.4	278	1	OX2G_RAT
13	124.5	7.2	365	1	CXAR_MOUSE
14	124	7.2	569	1	TACT_HUMAN
15	119.5	6.9	646	1	MU18_HUMAN
16	118.5	6.8	365	1	CXAR_HUMAN
17	114	6.6	837	1	NCM2_MOUSE
18	109	6.3	348	1	KILO_RAT
19	108.5	6.3	344	1	NTR1_RAT
20	106	6.1	243	1	CD48_HUMAN
21	105	6.1	335	1	SIAM_HUMAN
22	102	5.9	484	1	PAR2_XENLA
23	101.3	5.9	738	1	PAF_BOVIN
24	101	5.8	1274	1	BXF_CLOBO
25	100.5	5.8	337	1	G55A_CHICK
26	99	5.7	564	1	C166_BRARE
27	98.5	5.7	978	1	KFMS_FSVMD
28	97.5	5.6	285	1	FCG2_RAT
29	97.5	5.6	319	1	A33_HUMAN
30	97.5	5.6	978	1	KFMS_RAT
31	97	5.6	315	1	HEMA_VACCT
32	97	5.6	343	1	SIAM_MOUSE
33	96	5.5	246	1	MOG_BOVIN

ALIGNMENTS

RESULT 1	ID	CD86_HUMAN	STANDARD:	PRT:	329 AA.
34	96	5.5	246	1	MOG_MOUSE
35	95	5.5	417	1	PVR_HUMAN
36	94.5	5.5	583	1	C166_MOUSE
37	94.5	5.5	588	1	C166_CHICK
38	94.5	5.5	811	1	FS22_DROME
39	94.5	5.5	873	1	FS21_DROME
40	94.5	5.5	1900	1	STT4_YEAST
41	94	5.4	490	1	Y032_BORBU
42	94	5.4	964	1	DROL_CBEPV
43	93.5	5.4	245	1	MOG_RAT
44	93.5	5.4	345	1	OPCM_HUMAN
45	93.5	5.4	583	1	C166_HUMAN

CD86_HUMAN	1	CD86_HUMAN	STANDARD:	PRT:	329 AA.
AC	PA2081:	013655:			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	15-JUL-1998	(Rel. 36, Last annotation update)			
DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2				
DE	ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).				
GN	CD86 OR CD28LG2.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 94053735.				
RA	Freeman G.J., Gribben J.G., Boussoletis V.A., Ng J.W.,				
RA	Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;				
RT	"Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T				
RT	cell proliferation."				
RL	Science 262:909-911(1993).				
RN	[2]				
RP	SEQUENCE OF 7-329 FROM N.A.				
RX	MEDLINE: 94050123.				
RA	Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,				
RA	Lanier L.L., Somoza C.;				
RT	"B70 antigen is a second ligand for CTLA-4 and CD28."				
RL	Nature 366:76-79(1993).				
RN	[3]				
RP	SEQUENCE OF 7-329 FROM N.A.				
RC	TISSUE-FORESKIN.				
RX	MEDLINE: 95331831.				
RA	Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,				
RA	Green N.R., Gray G.S.;				
RT	"Genomic organization of the gene coding for the costimulatory human				
RT	B-lymphocyte antigen B7-2 (CD86)."				
RL	Immunogenetics 42:85-89(1995).				
RN	[4]				
RP	CHARACTERIZATION.				
RX	MEDLINE: 95088403.				
RA	Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,				
RA	Okumura K., Ito D., Azuma M.;				
RT	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T				
RT	cell proliferation, cytokine production, and generation of CTL."				
RL	J. Immunol. 154:97-105(1995).				
RN	[5]				
RP	IDENTIFICATION AS CD86.				
RX	MEDLINE: 94348060.				
RA	Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,				
RA	Nadler L.M., Wakasa H., Tedder T.F.;				
RT	"The B7-2 (B70) costimulatory molecule expressed by monocytes and				
RT	activated B lymphocytes is the CD86 differentiation antigen."				
RL	Blood 84:1402-1407(1994).				
CC	-1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL				
CC	FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY				
CC	BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY				

EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CELLS WITHIN 24 HOURS AFTER ACTIVATION.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
MONOCYTES.
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE C2-LIKE AND ONE V-LIKE DOMAINS.
-1- DATABASE: NAME-PROT; NOTE-CD guide CD86 entry;
WWW=HTTP://WWW.NCBI.NLM.NIH.GOV/PROT/CD/CD86.HTM"

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DR EMBL; L25259; AAA58389.1; -;
DR EMBL; U04343; AAB03814.1; -;
DR EMBL; U17722; AAA86473.1; -;
DR EMBL; U17717; AAA86473.1; JOINED.
DR EMBL; U17718; AAA86473.1; JOINED.
DR EMBL; U17719; AAA86473.1; JOINED.
DR EMBL; U17721; AAA86473.1; JOINED.
DR MIM; 601020; -;
DR INTERPRO; IPR000495; -;
DR PROSITE; PS00290; IG_MHC; FALSE; NEG.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
Receptor.
FT SIGNAL 1 23
FT CHAIN 24 329
FT DOMAIN 24 247
FT TRANSLEM 248 268
FT DOMAIN 329 329
FT DOMAIN 33 117
FT DOMAIN 149 225
FT DISULFID 40 110
FT DISULFID 157 218
FT CARBOHYD 33 33
FT CARBOHYD 47 47
FT CARBOHYD 135 135
FT CARBOHYD 146 146
FT CARBOHYD 154 154
FT CARBOHYD 177 177
FT CARBOHYD 192 192
FT CARBOHYD 213 213
FT CONFLICT 27 27
SQ SEQUENCE 329 AA; 37696 MW; 65DAF3826889CF7D CRC64;

Query Match 100.0%; Score 1733; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 2; 7e-125;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSLITLVMAFLISGAAPLKTIOAYFNETADLPQFANSONOSISELYVWQDQ 60
DB 1 MDPOCTMGLSLITLVMAFLISGAAPLKTIOAYFNETADLPQFANSONOSISELYVWQDQ 60
QY 61 ENLVANEVYLGKRFDSVSHKYMGRTSFDSDSMTLRLLNLQIKDKGLYCOCIIHKKKPTGM 120
DB 61 ENLVANEVYLGKRFDSVSHKYMGRTSFDSDSMTLRLLNLQIKDKGLYCOCIIHKKKPTGM 120
QY 121 IRIHOMNSEISVLANSOPETVPSINTEVNYINLCSSIHGHPKKKSVLLRTKNSSTI 180
DB 121 IRIHOMNSEISVLANSOPETVPSINTEVNYINLCSSIHGHPKKKSVLLRTKNSSTI 180
QY 181 EYDGIOMKSDONTVELKDVSISSVSPDVTSMNTIFCLIEDTKRLLSSPSIELEDDQ 240
DB 181 EYDGIOMKSDONTVELKDVSISSVSPDVTSMNTIFCLIEDTKRLLSSPSIELEDDQ 240
QY 241 PPPHIMWIRAVLPTVYICWVFCILIMKKKKRRRNSKTCNTNMEBESQTKRKREK 300
DB 241 PPPHIMWIRAVLPTVYICWVFCILIMKKKKRRRNSKTCNTNMEBESQTKRKREK 300

RESULT 2
CD86_RABIT
ID CD86_RABIT STANDARD; PRT; 330 AA.
AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
DE ANTIGEN).
GN CD86.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J X CHBB; HM;
RX MEDLINE; 95369849.
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
costimulatory molecules."
RT Immunogenetics 42:217-220(1995).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC BINDING CD80 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS.
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.

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DR EMBL; D49842; BAA08642.1; -;
DR INTERPRO; IPR000495; -;
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
Receptor.
FT SIGNAL 1 22
FT CHAIN 23 330
FT DOMAIN 23 247
FT TRANSLEM 248 268
FT DOMAIN 269 330
FT DOMAIN 33 117
FT DOMAIN 149 225
FT DISULFID 40 110
FT DISULFID 157 218
FT CARBOHYD 33 33
FT CARBOHYD 135 135
FT CARBOHYD 146 146
FT CARBOHYD 154 154
FT CARBOHYD 177 177
FT CARBOHYD 192 192
FT CARBOHYD 213 213
FT CONFLICT 27 27
SQ SEQUENCE 330 AA; 37142 MW; 935CD65C57E3EE1 CRC64;

Query Match 55.6%; Score 963.5; DB 1; Length 330;

QY 241 PPPHIMWIRAVLPTVYICWVFCILIMKKKKRRRNSKTCNTNMEBESQTKRKREK 300
DB 241 PPPHIMWIRAVLPTVYICWVFCILIMKKKKRRRNSKTCNTNMEBESQTKRKREK 300

CC RECEPTOR.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: D49843; BAA08643.1; -
 CC INTERPRO: IPR003006; -
 CC PFAM: PF00047; 1g; 1.
 CC Immunoglobulin domain; T-cell; Glycoprotein; signal; Transmembrane;
 CC Receptor.
 CC FT SIGNAL 1 32 POTENTIAL.
 CC FT CHAIN 33 299 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
 CC FT DOMAIN 33 243 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 244 264 POTENTIAL.
 CC FT DOMAIN 265 299 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 42 122 IG-LIKE V-TYPE DOMAIN.
 CC FT DOMAIN 154 222 IG-LIKE C2-TYPE DOMAIN.
 CC FT DISULFID 49 115 POTENTIAL.
 CC FT DISULFID 161 215 POTENTIAL.
 CC FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 165 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 299 AA; 33513 MW; 6744223ECC91DE0 CRC64;

Query Match 14.0%; Score 243; DB 1; Length 299;
 Best Local Similarity 25.8%; Pred. No. 1,1e-11;
 Matches 81; Conservative 65; Mismatches 122; Indels 46; Gaps 14;

3 POSTMTGLSNLFMAFLSCAPLKIQAAYFNETADLPQCFANSONSLSELVFMDOEN 62
 12 PRLHLKLCILLALAGHPSGSGISQYTKSKEMALSCDY NISIDELARMTYMKDXX 70
 63 LVINEVYLKKEKFDVSHKMGRTSPD-SDSWTLRLHNIQIKDKGLYOCIIHKKPTGMI 121
 71 MWLS-IISGVE--VWPEKKNRTFPDIINNLIMLIALRLSDKGTTCVQKENGSGFR 126
 122 RIHQMSSESVLANFSOPEIYVPSINTENYINLTGSSSHGYDEPK---KMSVLLRTKN 177
 127 REHLTSTVLSIRADFPPPSITDIGHDPNPK-RIRCSASGSGPEPRLAMWDEGEELNAYN 185
 178 STEYDQIMQSDQNTVELYDVISLSVSPDYSNMNTIFCIETETKTRLLSSPSIELE 237
 186 TTYD-----QDLDELKYSSELD---NTNNHSYICLKYGELS-VSGIIFWMSKP 233
 238 DPOPPDHIP-WITAVLPT---VITCVWFCLL---LWKKKKKRRPRNSYKCGTNTMER 289
 234 KOEPPIDQLPFVW--IIPVSGALVLTAVLVYLCLACHVAMKRRTR-----N 278
 290 EESQTKKKREKIH 303
 279 EEYGVTERLSPIYL 292

RESULT 6
 CD80_HUMAN STANDARD; PRT; 288 AA.
 AC P33681;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1
 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.1) (B7) (BB1).
 GN CD80 OR CD28LG1 OR CD28LG OR LAB7.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOID.
 RA MEDLINE: 90010147.
 RA Freeman G.J., Freedman A.S., Segal J.M., Lee G., Whitman J.F.,
 RA Nadler L.M.;
 RA "B7, a new member of the Ig superfamily with unique expression on
 RT activated and neoplastic B cells.";
 RL J. Immunol. 143:2714-2722(1989).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92307753.
 RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
 RA Dupont B.;
 RA "Genomic organization and chromosomal location of the human gene
 RT encoding the B-lymphocyte activation antigen B7.";
 RL Immunogenetics 36:175-181(1992).
 RN [3]
 RP SEQUENCE OF 35-38.
 RX MEDLINE: 91341422.
 RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
 RA White M., Fingerhuth J.D., Grubben J.G., Nadler L.M.;
 RA "Structure, expression, and T cell costimulatory activity of the
 RT murine homologue of the human B lymphocyte activation antigen B7.";
 RL J. Exp. Med. 174:625-631(1991).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE: 95088403.
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RA "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 RL [5]
 RP FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
 CC AND DENDRITIC CELLS.
 CC -1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -1 DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
 CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD80.HTM".
 CC -----
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 CC -----
 CC EMBL: M27533; AAA36045.1; -
 CC EMBL: M83077; AAA58390.1; -
 CC EMBL: M83072; AAA58390.1; JOINED.
 CC EMBL: M83073; AAA58390.1; JOINED.
 CC EMBL: M83074; AAA58390.1; JOINED.
 CC PIR: A45803; A45803.
 CC MIM: 112203; -
 CC DR INTERPRO: IPR003006; -
 CC DR PFAM: PF00047; 1g; 1.
 CC Immunoglobulin domain; T-cell; Glycoprotein; signal; Transmembrane;
 CC Receptor.
 CC FT SIGNAL 1 34
 CC FT CHAIN 35 288 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
 CC FT DOMAIN 35 242 EXTRACELLULAR (POTENTIAL).

Query Match 11.6%; Score 201.5; DB 1; Length 288;
Best Local Similarity 25.1%; Pred. No. 1.5e-08;
Matches 78; Conservative 57; Mismatches 109; Indels 67; Gaps

FT	TRANSMEM	263	POTENTIAL.
FT	DOMAIN	264	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	43	IG-LIKE V-TYPE DOMAIN.
FT	DOMAIN	155	IG-LIKE C2-TYPE DOMAIN.
FT	DISULFID	50	POTENTIAL.
FT	DISULFID	162	POTENTIAL.
FT	CARBOHYD	53	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	89	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	98	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	186	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	207	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	211	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	226	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	232	N-LINKED (GLCNAC. . .)
SO	SEQUENCE	288 AA; 33048 MW; BA453BE34528B1F4 CRC64;	

Query Match 11.6%; Score 201.5; DB 1; Length 288;
Best Local Similarity 25.1%; Pred. No. 1.5e-08;
Matches 78; Conservative 57; Mismatches 109; Indels 67; Gaps

FT	TRANSMEM	263	POTENTIAL.
FT	DOMAIN	264	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	43	IG-LIKE V-TYPE DOMAIN.
FT	DOMAIN	155	IG-LIKE C2-TYPE DOMAIN.
FT	DISULFID	50	POTENTIAL.
FT	DISULFID	162	POTENTIAL.
FT	CARBOHYD	53	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	89	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	98	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	186	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	207	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	211	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	226	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	232	N-LINKED (GLCNAC. . .)
SO	SEQUENCE	288 AA; 33048 MW; BA453BE34528B1F4 CRC64;	

[illegible]


```

Db 45 LGSPGLLEFLFSSLRADTQOEKVRAMVGSVDVLESCAPCEGSRFDLNDVYVWQTSSEKTV 104
QY 66 NEVYLGK-EKPDVSHKMGRTSPD-----SDSMTLRLHNIQIDKGLYCIITHHKPTG 119
Db 105 VTHIIPDNSSLENDVSRIRNRLALMSPAGMLRGDPSLRLEFNTVPDDEQFHCIV-LSOSLG 163
QY 120 MIRIHMNSSEVLANSOPEIPIVPSINTENVYINLNCSSIHGYPEPKMSVLLRTKST 179
Db 164 FOEVLSEVTLHVAANSVP-VVSAPHSPPODELFTCTISNGYPRP-NVYWKTDNSL 221
QY 180 IENDGIMQKSOD-----NTELYVVSISLSVSPDVTSMNITFCILET----- 222
Db 222 LD-----QATQNDTVFIMRGLXDVSVLRIA---RTPSVNIGCCIEENVLLQNLTVGSQ 273
QY 223 -----DKTRLSSPFSFIEEDPPPPDHIPW-ITAVIPYIIVMPCILMMKKKKR 275
Db 274 TGNDIGERDKITENPVSTGEKNA-----ATWSILAVL-----CLLVVAVAIAGWVCCR 322

RESULT 10
BUTY_BOVIN STANDARD; PRT; 526 AA.
AC P18892; O18955; O18959;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
GN BTN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE: 90354441.
RA Jack L.J.W., Mather I.H.;
RT "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical
RT glycoprotein expressed in mammary tissue and secreted in association
RT with the milk-fat globule membrane during lactation.";
RL J. Biol. Chem. 265:14481-14486(1990).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN-FRIESIAN;
RA Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,
RA Mather I.H., Wilkins R.J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA Seyfert H., Luethen F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RN CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE: 95293916.
RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
RT "Site-specific glycosylation of bovine butyrophilin.";
RL J. Biochem. 117:147-157(1995).
RN [5]
RN FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
RN MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
RN ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
RN MEMBRANE.
CC -1 SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC ASSOCIATION WITH THE MILK-FAT GLOBULE MEMBRANE DURING LACTATION.
CC -1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
CC -1 SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).
CC -----
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CC -----
DR EMBL: M35551; AAB39766.1; -.
DR EMBL: AF005497; AAB62889.1; -.
DR EMBL: Z93323; CAB07533.1; -.
DR PIR: A37821; A37821.
DR INTERPRO: IPR00107; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00622; SPRY. 1.
DR PFAM: PF00047; Ig. 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 27
FT DOMAIN 27 526
FT TRANSMEM 243 269
FT DOMAIN 270 526
FT CARBOHYD 55 55
FT CARBOHYD 215 215
FT CONFLICT 35 35
FT CONFLICT 230 230
SQ SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;

Query Match 9.38; Score 162, DB 1; Length 526;
Best Local Similarity 23.08; Pred. No. 3,4e-05;
Matches 80; Conservative 61; Mismatches 155; Indels 52; Gaps 16;

QY 5 CTMGLSNLFLYMAVLISGAAPL-----KIQAYFNFETADLPQOFANSONSLSEIVFW 57
Db 8 CLAGCLIFILIQPKLDSAPFDVIGQEPQLAVVAGEDALPCRL--SPNYSAGKMELRW 65
QY 58 QDQENLVLENYL--GKEKFDVSHKMGRTSPSD-----SMTLRHNLQIDKGLYQ 109
Db 66 FREK--VSPAVFVREGQEOGGEEMAEYRGVSLVEDHIAGSVAVRLQEVKASDDGEYR 123
QY 110 CIHHKPTGIGIRHOMNSSEVLANSOPEIPIVPSINTENVYINLNCSSIHGYPEPKM 169
Db 124 CFFRQDENYEBAIVH-----LKVALGSDPHI--SMKVOESGELQLCTSGVWPEPO-- 174
QY 170 SVLLRTKSTLEYDGIQKSODNVTLEYDVSISSVSPDVTSMNITFCILETDTKRLS 229
Db 175 -VQRTIRHGE-EFPPSMESNRNPDEGLF--TVRSVYIIRSSMKMNVSCCI-----RNLLG 226
QY 230 SPFSIELEDDPP-PPDHIPMITAV-LPTVIICVWFCLILMKK---KKRPRNSYKCG 283
Db 227 QKEKEVVISIPASFPRLTPMVAVALVILVGLTIGISIFFTWRLYKERSQRNRNEF--- 283
QY 284 TMTMERESQTKKREKIH-----PERSDQARVYKSKTSKDCDS 325
Db 284 -SSKEKLEELKMKRATLVAVDTLPDPTAHPLILEYEDSKSVRLDS 330

RESULT 11
OX2G_HUMAN STANDARD; PRT; 274 AA.
ID OX2G_HUMAN
AC P41217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).
GN MOX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE: 87192943.
RA McCaughan G.W., Clark M.J., Barclay A.N.;
RT "Characterization of the human homolog of the rat MRC OX-2 membrane

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RT glycoprotein."
RL Immunogenetics 25:329-335(1987).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE IMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND ONE C2-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: X05323; CAA28943.1; ALT. SEQ.
DR EMBL: X05324; CAA28943.1; JOINED.
DR EMBL: X05325; CAA28943.1; JOINED.
DR EMBL: X05326; CAA28943.1; JOINED.
DR PIR: A47639; A47639.
DR MIM: 155970; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig 2.
KW Transmembrane; Glycoprotein; Neurone; B-cell; T-cell; Antigen;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 274
FT DOMAIN 27 228
FT TRANSMEM 229 255
FT DOMAIN 256 274
FT DOMAIN 27 137
FT DOMAIN 138 228
FT DISULFID 47 117
FT CARBOHYD 156 210
FT CARBOHYD 99 91
FT CARBOHYD 106 106
FT CARBOHYD 133 153
FT CARBOHYD 177 177
FT CARBOHYD 186 186
SO SEQUENCE 274 AA; 30739 MW; 0A9547B48BD8979C CRC64;

Query Match 7.4%; Score 128; DB 1; Length 274;
Best Local Similarity 21.1%; Pred. No. 0.0058;
Matches 63; Conservative 57; Mismatches 120; Indels 58; Gaps 16;

QY 11 NILEFVAFILSGAFLKI-----QAYFNETADLPQOFANSQNSLSLVEFWQDQ--- 60
DB 13 SLVWMAVAVLCITRAOVAVTODEREDLY--TTSLSKCSLQNAQ-----EALIVTWQKKAV 66
QY 61 --ENLVL-----NEVYLKEKEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIHH 114
DB 67 SPEPMVTFSENHGVVIOIPAYKDKINITOLGQNSTITFW-----NITLEDGCGMCLFN- 120
QY 115 KKPGLGMRIHOMNSELVLANFQSPETIPIPSNITENYINLTCSSIHGVEPKMSYLRL 174
DB 121 --TFGFKI-----SGTACILVYQVOP-IVSLHYKFSEDHLNITCSAT-ARAP---MYFWK 169
QY 175 TKNSTIEEDGIMQSDNTELYDVSTISLSVSPDYTSNMTITFC-ILE-----TDKTRLLS 229
DB 170 VPRSGIENSTYTLISHRNGTTSVSI---LHKDKPKNOVGKEVICOVLYHLGTVDKQTVN 226
QY 230 SPFSIELEDQPPPDHILPWITAVLPYIIVCWVFCILMKWKKKKRRPNRSYKCGTNTM 287
DB 227 KGYWES-----VPLLSTIVSLVILVILSLILYWK-RHRNDQRGELISQGVOKM 273

RESULT 12
OX2G_RAT STANDARD; PRT; 278 AA.
AC P04218;
DT 20-MAR-1987 (Rel. 04, Created)

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DT 20-MAR-1987 (Rel. 04, last sequence update)
DE 15-JUL-1999 (Rel. 38, last annotation update)
DE OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (MRC OX-2 ANTIGEN).
GN MOX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85257428.
RA Clark M.J., Gagnon J., Williams A.F., Barclay A.N.;
RT "MRC OX-2 antigen: a lymphoid/neuronal membrane glycoprotein with a
RT structure like a single immunoglobulin light chain."
RL EMBO J. 4:113-118(1985).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND ON THE SURFACE OF NEURONES, THYMOCYTES,
CC B-CELLS, AND FOLLICULAR DENDRITIC CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND ONE C2-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: X01785; CAA25925.1; -.
DR PIR: A02114; TDRTOX.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig 2.
KW Transmembrane; Glycoprotein; Neurone; B-cell; T-cell; Antigen;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 30
FT CHAIN 31 278
FT DOMAIN 31 232
FT TRANSMEM 233 259
FT DOMAIN 260 278
FT DOMAIN 31 141
FT DOMAIN 142 232
FT DISULFID 51 121
FT CARBOHYD 160 214
FT CARBOHYD 95 95
FT CARBOHYD 103 103
FT CARBOHYD 110 110
FT CARBOHYD 157 157
FT CARBOHYD 181 181
FT CARBOHYD 190 190
SO SEQUENCE 278 AA; 31088 MW; B5A72DBE7B3116CD CRC64;

Query Match 7.4%; Score 128; DB 1; Length 278;
Best Local Similarity 22.1%; Pred. No. 0.0059;
Matches 70; Conservative 53; Mismatches 128; Indels 66; Gaps 16;

QY 3 POCMGLSILFLVMAFLSGAFLKI-----QAYFNETADLPQOFANSQNSLSLVEFW 57
DB 9 PFOHLSSTILMAIAVALSTQAVEVVTODERKLLHTTASLSKSLTKTQ---EPLIVTW 64
QY 58 QDO-----ENLV-----LNEVYLKEKEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLY 108
DB 65 QKKKAVGPENMYYSKAGHVIOIPYKDKINITEGLTFTSTFW-----NITLEDGCGY 119
QY 109 OCTLIHKKPGLGMRIHOMNSELVLANFQSPETIPIPSNITENYINLTCSSIHGVEPKK 168
DB 120 MCLF-NMFGSGKY-----SGTACILVYQVPIVHLHYNFED-HLNTCSAT-ARAP-- 168
QY 169 MSVYLKTKNSTIEDGIMQSDNTELYDVSTISLSVSPDYTSNMTITFCIL-----ETD 223
DB 169 -AISWKGTSGISIE-NSTESHSHNGTT--SVTSILRYKDKPKQVGKEVICOVLYLGNVID 224
QY 224 KTRLLSPFSIELEDQPPPDHILPWITAVLPYIIVCWVFCILMKWKKKKRRPNRSYKCG 283

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Db 225 YKQSLDKGFMS-----VPLLSIVYLIVLISILYX-----KRRRN----- 264

QY 284 TMTERESEGTKKRK 300

Db 265 --OERGESSOGOMRMK 278

RESULT 13

CDX_MOUSE STANDARD; PRT; 365 AA.

AC P97792; 009052;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR HOMOLOG PRECURSOR (MCAR).

GN CXADR OR CAR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=LIVER;

RX MEDLINE: 97190109.

RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Kitthivas A., Hong J.S., Horvitz M.S., Crowell R.L., Finberg R.W.;

RT "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."

RL Science 275:1320-1323(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/MAI;

RX MEDLINE: 97250541.

RA Tomko R.P., Xu R., Phillips L.;

RT "MCAR: The human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses."

RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=LIVER;

RA Bergelson J.M., Kitthivas A., Crowell T.L., Finberg R.W.;

RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B viruses and adenoviruses."

RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC -----

DR EMBL: Y10320; CAA71368.1; -

DR EMBL: U90715; AAC53148.1; -

DR EMBL: Y11929; CAA72679.1; -

DR MGD: MGI:1201679; CXADR.

DR INTERPRO: IPR003006; -

DR PFM: PFM00047; 1g; 2.

KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 19

FT CHAIN 20 365

FT COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR

FT HOMOLOG.

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 238 258

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 259 365

FT DOMAIN 34 127

FT DOMAIN 155 219

FT DISULFID 41 120

FT DISULFID 162 212

FT CARBOHYD 106 106

N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL)

FT CONFLICT 340 365

FT VAPNLSRGAAPVATIPKQSDGSLV -> FRIATKIDGIT

FT VV (IN REF. 2 AND 3).

FT 5445BAH52A34B2A2 CRC64;

SO SEQUENCE 365 AA; 39947 MW; 5445BAH52A34B2A2 CRC64;

Query Match

Best Local Similarity 24.6%; Pred. No. 0.015;

Matches 78; Conservative 49; Mismatches 125; Indels 65; Gaps 17;

7.2%; Score 124.5; DB 1; Length 365;

QY 27 KIQAFNEIADLPQOPANS-QNOSLSELVFWODENLVNEV---YLGKEKEDSVHSKY 82

Db 28 RIEKAKGETAYLPCKFKLSPEDOGPDIDMLISPSDNOIVDQVILYSQDKYDVPYDYL 87

QY 83 MGRFSPSD-----SWTLRHNIOIKDKGYOCIIHKKRPTQMIRHONSLSLVANFS 137

Db 88 KGRHFTSNVKGSDASINTNQLSDIGTYCKV--KAPG---VANKKFLILVAVPS 142

QY 138 QPE-IVPISNITENVYINLTGSSIHGYPEPKMSVLLRKNSTIEYDGIKQSDNVT-- 194

Db 143 GTRCFVDSGEIGNDF-KLKC-----EPKEGSLPEPE-----WOKLSDSQTMP 185

QY 195 -----ELYDVISISVSFPPDYSNMNITFCLLEPDKTRLLSPFSELEDDPPPHIPI 249

Db 186 TPWLAEMTSFYISKNAISYSG--TYSC---TVQNRVSDCMLRL-DVPPSPRAGTI 239

QY 250 T-AVLPTVITCVV---FCLILMKWKKRKRPNRSYKSGTMTERESEGTKKRKIHIP 304

Db 240 AGAVIGITLALVILGALIFCC-----HRRKREKY-----EKEVHHDREDVPP 284

QY 305 ERSDAQRFKSKTS 321

Db 285 KSRITSTARSTIGSNHS 301

RESULT 14

TACT_HUMAN STANDARD; PRT; 569 AA.

AC P40200;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).

GN CD96.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 92218864.

RA Wang P.L., O'Farrell S., Clayberger C., Krensky A.M.;

RT "Identification and molecular cloning of tactile, A novel human T cell activation antigen that is a member of the Ig gene superfamily."

RL J. Immunol. 148:2600-2608(1992).

CC -1- FUNCTION: MAY BE INVOLVED IN ADHESIVE INTERACTIONS OF ACTIVATED T AND NK CELLS DURING THE LATE PHASE OF THE IMMUNE RESPONSE. MAY FUNCTION AT A TIME AFTER T AND NK CELLS HAVE PENETRATED THE ENDOTHELIDUM USING INTEGRINS AND SELECTINS, WHEN THEY ARE ACTIVELY ENGAGING DISEASED CELLS AND MOVING WITHIN AREAS OF INFLAMMATION.

CC -1- SUBUNIT: HOMODIMER, LINKED BY A DISULFIDE BOND.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED ON NORMAL T CELL LINES AND CLONES, AND SOME TRANSFORMED T CELLS, BUT NO OTHER CULTURED CELL LINES.

CC TESTED. IT IS EXPRESSED AT VERY LOW LEVELS ON ACTIVATED T CELLS.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT LOW LEVELS ON PERIPHERAL T CELLS AFTER THE ACTIVATING STIMULUS.

CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -1- DATABASE: NAME=PROM, NOTE=CD guide CD96 entry.

CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROM/CD/CD96.htm".

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CC EMBL: M8282; AAA5662.1; -

DR PIR: A46462; A46462.

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 19; 3. Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 569 T-CELL SURFACE PROTEIN TACTILE.

FT DOMAIN 22 501 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 502 525 POTENTIAL.

FT DOMAIN 526 569 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 534 486 PRO/SER/THR-RICH.

FT DOMAIN 538 547 PRO-RICH.

FT DOMAIN 538 125 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 156 238 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 267 346 IG-LIKE C2-TYPE DOMAIN.

FT DISULFID 45 118 PROBABLE.

FT DISULFID 163 231 PROBABLE.

FT DISULFID 274 339 PROBABLE.

FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 569 AA; 63887 MW; DF2F3BEE356F3BF2 CRC64;

Query Match 7.28; Score 124; DB 1; Length 569;

Best Local Similarity 25.3%; Pred. No. 0.03;

Matches 63; Conservative 44; Mismatches 96; Indels 46; Gaps 15;

QY 28 IQAYFNETADLPQFANSONOSISLVFWQDENLVLENYVYGRKRPDSVHSGMGRTS 87

DB 151 IELEINOTLEIPC-FOUSSKISSSEFYAMSVEDN-GTQETLISONHLISNTLLADRYK 208

QY 88 FDSDSWTLRLNLIQDKG-LYOCIIHKKRPTGMIRIHONSELVLANSOPEI-VPIS 145

DB 209 LGTD-YELHLSPOYFDGRKFSCHIR---VGNKILRSTTVKV---FAKPEIPIYVE 260

QY 146 NITENVTI--NLRCSSHGPRPKKMSVLLRTKNTI--TYDGIM-----QKQDOWTE 196

DB 261 NNSDVLVERFRCTCLKNVP--KANITWFDGSLHDKREGIYITNEERKGDGFL 317

QY 197 YDVSISISVSPPDVTSMNTEFCI-----LETDK-TRLLSS-----PSI-- 234

DB 318 KSVLTTRHNSKRPASDMLTWCAALSVPPNKYNNISSEKITPILGSEISSTDPPLSYTE 377

QY 235 ELEDOPPP 243

DB 378 STLDTPSP 386

QY 235 ELEDOPPP 243

DB 378 STLDTPSP 386

QY 235 ELEDOPPP 243

DB 378 STLDTPSP 386

QY 235 ELEDOPPP 243

DB 378 STLDTPSP 386

QY 235 ELEDOPPP 243

DB 378 STLDTPSP 386

QY 235 ELEDOPPP 243

DB 378 STLDTPSP 386

QY 235 ELEDOPPP 243

DB 378 STLDTPSP 386

QY 235 ELEDOPPP 243

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN

MUC18) (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL-

DE ASSOCIATED ANTIGEN) (CD146 ANTIGEN) (MELANOMA ADHESION MOLECULE).

GN MAM OR MUC18

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RC [1]

RP SEQUENCE FROM N.A.

RC TISSUE-MELANOMA:

RX MEDLINE; 90099368.

RA Leuermann J.M., Riettmueller G., Johnson J.P.;

RT "MUC18, a marker of tumor progression in human melanoma, shows

RT sequence similarity to the neural cell adhesion molecules of the

RT immunoglobulin superfamily.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:9891-9895(1989).

RN [2] REVISIONS. SEQUENCE FROM N.A.

RP TISSUE-MELANOMA:

RC MEDLINE; 93391384.

RA Sers C., Kirsch K., Rothbacher U., Riettmueller G., Johnson J.P.;

RT "Genomic organization of the melanoma-associated glycoprotein MUC18:

RT implications for the evolution of the immunoglobulin domains.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:8514-8518(1993).

RN [3] SEQUENCE OF 24-44; 98-112; 135-153; 240-260; 379-389 AND 460-478.

RP MEDLINE; 94215196.

RA Shih I.-M., Eleder D.E., Speicher D., Johnson J.P., Herlyn M.;

RT "Isolation and functional characterization of the A32 melanoma-

RT associated antigen.";

RL Cancer Res. 54:2514-2520(1994).

RN [4] SEQUENCE OF 27-40; 98-112 AND 236-260.

RP MEDLINE; 9616302.

RA Bardin N., Frances V., Lesaulle G., Horschowski N., George F.;

RT "Identification of the S-Endo 1 endothelial-associated antigen.";

RL Biochem. Biophys. Res. Commun. 218:210-216(1996).

RN [5] FUNCTION.

RP MEDLINE; 94122526.

RA Johnson J.P., Rothbacher U., Sers C.;

RT "The progression associated antigen MUC18: a unique member of the

RT immunoglobulin supergene family.";

RL Melanoma Res. 3:337-340(1993).

CC -I- FUNCTION: COULD BE AN ADHESION MOLECULE ACTIVE IN NEURAL CREST

CC CELLS DURING EMBRYONIC DEVELOPMENT. ITS EXPRESSION MAY ALLOW

CC MELANOMA CELLS TO INTERACT WITH CELLULAR ELEMENTS OF THE VASCULAR

CC SYSTEM THEREBY ENHANCING HEMATOGENOUS TUMOR SPREAD.

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- TISSUE SPECIFICITY: MAY APPEAR AT THE SURFACE OF NEURAL CREST

CC CELLS DURING THEIR EMBRYONIC MIGRATION. APPEARS TO BE LIMITED TO

CC VASCULAR SMOOTH MUSCLE IN NORMAL ADULT TISSUES. ASSOCIATED WITH

CC TUMOR PROGRESSION AND THE DEVELOPMENT OF METASTASIS IN HUMAN

CC MALIGNANT MELANOMA. EXPRESSED MOST STRONGLY ON METASTATIC LESIONS

CC AND ADVANCED PRIMARY TUMORS AND IS ONLY RARELY DETECTED IN BENIGN

CC MELANOCYTIC NEVI AND THIN PRIMARY MELANOMAS WITH A LOW PROBABILITY

CC OF METASTASIS.

CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

CC 3 C2-LIKE AND 2 V-LIKE DOMAINS.

CC -I- DATABASE: NAME-PROV: NOTE-CD guide CD146; HTW".

CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CD146.HTW".

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Db 184 DTVMKSSNNVTETLYNSISLSFSVPE-ASNVSIFCVLOLESWKLPSPLYNIDATKPRP 242
 QY 242 PRDHIPITAVL-PTVICVWFCLIMKKKKKKRPNRYKCGTNTMEHESEQTKRK 300
 Db 243 DGDHILMIALVLMVLCGMFFTLTK-RKKQKOPSHCECTNKVERKESEQTKERV 301
 QY 301 IHIPERSDEAORVFKSSKTSKSDKSDTCE 329
 Db 302 YHETERSDEACV-NISKTSAGDNSTTOF 329

RESULT 2

002838 PRELIMINARY; PRT; 325 AA.
 ID 002838
 AC 002838;
 DT 01-JUL-1997 (TREMBREL. 04, Created)
 DT 01-JUL-1997 (TREMBREL. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBREL. 10, Last annotation update)
 DE CD86.
 GN Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97047772.
 RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
 RA Botwell A.L.;
 RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human
 RT T cells: cloning, sequencing, and functional expression in human
 RT endothelial cells."
 RL J. Immunol. 157:3838-3844(1996).
 DR EMBL: L76099; AAB61307.1; -
 SQ SEQUENCE 325 AA; 36527 MW; 98BBE08137B0597D CRC64;

Query Match 55.0%; Score 953; DB 6; Length 325;
 Best Local Similarity 61.4%; Pred. No. 7.7e-74;
 Matches 202; Conservative 44; Mismatches 73; Indels 10; Gaps 8;

QY 7 MGLSNILFVMAFLISGAAPLKIOAFNETADLPQFANSQNSISLTVFMDQENLYN 66
 Db 1 MGLSNILFVMAFLISGAAPLKIOAFNETADLPQFANSQNSISLTVFMDQENLYN 66
 QY 67 EYVLGKKEPDSVHSKYMGRTSFDSDSWTLRLNLIQIKDKGLYOCIIHKKPTGIRIHO 126
 Db 61 ELYGQKPPHNVNSKYMGRTSFDQATWTLRLHNVOIKDKGSYOCFIIHKGPIVPIHO 120
 QY 127 NSELSTLANFSOPETIVISNTENYINILGSSIHGYPPEKKKSVLLRTKNTIEYDGI 186
 Db 121 SSDLSILANFSOPETINLHTNSVYNILGSSISOGYPPEKRYMLLNTKNTTTHDAD 180
 QY 187 QKSDONTVELDYVSISSVSPDVTSMNTIFCI-LETDTKRLSSPSFIEEDP-OPP- 242
 Db 181 KKSQNTITELYNSISIRSLPIPET-NVSIIVCYLOLEPSKTLFLSPCIDAKKPPVQPV 239
 QY 243 PDHITPITAVLP-VIICVWFCLIMKKKKRPNRYKCG-TNMEHESEQTKRK 300
 Db 240 PDHILMIALVLMVLCGMFFTLTK-RKKQKOPSHCECTNKVERKESEQTKERV 298
 QY 301 IHIPERSDEAORVFKSSKTSKSDKSDTCE 329
 Db 299 VH-ERSDQAQCVNLIKTSADNSTTDF 325

RESULT 3
 Q9XSX6 PRELIMINARY; PRT; 329 AA.
 ID Q9XSX6
 AC Q9XSX6;
 DT 01-NOV-1999 (TREMBREL. 12, Created)
 DT 01-NOV-1999 (TREMBREL. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBREL. 12, Last annotation update)
 DE C86 ANTIGEN.

GN CD86.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi I.-S., Hash S., Winslow B.J., Collisson E.W.;
 RT "Sequence analyses of feline B7 costimulatory molecules."
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF157827; AAD42974.1; -
 SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08BB CRC64;

Query Match 52.1%; Score 903; DB 6; Length 329;
 Best Local Similarity 58.5%; Pred. No. 1.5e-69;
 Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

QY 6 TMGLSNILFVMAFLISGAAPLKIOAFNETADLPQFANSQNSISLTVFMDQENLYN 65
 Db 7 TMGLSNILFVMAFLISGAAPLKIOAFNETADLPQFANSQNSISLTVFMDQENLYN 66
 QY 66 NEYVLGKKEPDSVHSKYMGRTSFDSDSWTLRLNLIQIKDKGLYOCIIHKKPTGIRIHO 125
 Db 67 YELFRKENPQNVHLKYKRTSPDKMWTLRHLNVOIKDKGYHCFIHYKPKGLVPIHO 126
 QY 126 NSELSTLANFSOPETIVISNTENY-YNILGSSIHGYPPEKKKSVLLRTKNTIEYD 184
 Db 127 MSSDLSILANFSOPETIVISNTENYINILGSSISOGYPPEKRYMLLNTKNTTTHDAD 186
 QY 185 IMKSDONTVELDYVSISSVSPDVTSMNTIFCI-LETDTKTR-LSSPSFIEEDP-DPO 241
 Db 187 VMKSSNNVTETLYNSISLSFSVPE-AHNVSYFCAIKLETLMLSLPFDNDAQPKKDP 245
 QY 242 PRDHIPITAVLP-VIICVWFCLIMKKKKRPNRYKCGTNTMEHESEQTKRK 300
 Db 246 EOGHFLMIAVLMVLCGMFFTLTK-RKKQKOPSHCECTNKVERKESEQTKERV 304
 QY 301 IHIPERSDEAORVFKSSKTSKSDKSDTCE 325
 Db 305 YHETERSDEACV-NIKTSAGDNK 328

RESULT 4
 Q9TFF1 PRELIMINARY; PRT; 280 AA.
 ID Q9TFF1
 AC Q9TFF1;
 DT 01-MAY-2000 (TREMBREL. 13, Created)
 DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBREL. 14, Last annotation update)
 DE TRUNCATED B7-2 PROTEIN.
 GN CD86.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang S., Sim G.-K.;
 RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
 RT Molecules."
 RL Immunogenetics 50:349-353(1999).
 DR EMBL: AF106827; AAF17298.1; -
 DR INTERPRO: IPR000495; -
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1
 SQ SEQUENCE 280 AA; 32265 MW; 3C6BCA4D826A7F3 CRC64;

Query Match 51.2%; Score 886.5; DB 6; Length 280;
 Best Local Similarity 55.7%; Pred. No. 3.1e-68;
 Matches 182; Conservative 40; Mismatches 54; Indels 51; Gaps 4;

QY 4 QCTMGLSNILFVMAFLISGAAPLKIOAFNETADLPQFANSQNSISLTVFMDQENLYN 63
 Db 4 RCTMGLSNILFVMAFLISGAAPLKIOAFNETADLPQFANSQNSISLTVFMDQENLYN 63

OY		64	VINEYLGNKFNDFSVHKKMGRTSFPDSMTLTLLHLNLOIKDKGLQCIHHHKRPPGMIRI	123
Dd		64	VVLEYELRGKNPNVNHRKYRKTSFDDKDNTLNLHNIOIKDGLVCVCHHGPRGVLPM	123
OY		124	HOMNSLSLVNFSPPELVPISNTENV-VYNLCSSIGGYEPKMSVALTRTKNSTLEY	182
Dd		124	HOHNSDLSTANFSOPPELMWTSNTENSGLINLTCSIGGYEPKEMFVLKTENMSTRY	183
OY		183	DGIIMOKSDONVTALDYDISLSVSFDPVYSNMTFICILETDTRLISSPFILEDPOP	247
OY		184	DVMKKSQNNWTETLYXNISISLSFSVPE-ASNVSFICQLIESMKPLPSLENYNE-----	235
OY		243	PDHPIPTAVLPVTITCYMWFCILMMKKKKRRNRMSYKGCGTFTMRESEDTKKREKI	302
Dd		236	-----TNKVRKKSDEQKERVKXH	257
OY		303	IIPERSDAORFKSKTSCTSCDKSDTCF	329
Dd		255	ETERSDACOV-NISKTSNGDNSTTOE	280
RESULT	5			
ID	061238	PRELIMINARY;	PTH:	314 AA.
AC	061238:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
De	T CELL COSTIMULATORY MOLECULE B7-2.			
GN	CD86 OR B7-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129;			
RX	MEDLINE F, Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;			
RA	Bortelleo P., Oliveros J.,			
J	"Differential expression of alternate mb7-2 transcripts."			
RL	J. Immunol. 155:5490-5497(1995).			
DR	EMBL: U39456; AAC52335.1; -			
DR	EMBL: U39460; AAC52335.1; JOINED.			
DR	EMBL: U39461; AAC52335.1; JOINED.			
DR	EMBL: U39462; AAC52335.1; JOINED.			
DR	EMBL: U39463; AAC52335.1; JOINED.			
DR	EMBL: U39464; AAC52335.1; JOINED.			
DR	EMBL: U39465; AAC52335.1; JOINED.			
DR	EMBL: U39466; AAC52335.1; JOINED.			
DR	MGJ: MG1:101773; Cd86.			
SQ	SEQUENCE	314 AA:	35177 MW:	3D2683F36CADEDEF4 CRC64;

[illegible]

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QY 245 HLPW--TAVLEPTVICWVFCILMKKKKKRPNRSTKCTNINMEEDESQTKREKH 302
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 245 QTYMEITASTAVALLVWL--LIIVCHKKNOPSRP---SNTASKLERDSNADRETIN 298
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 303 IPE 305
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 LKE 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT	ID	PRELIMINARY:	PRF:	356 AA.
064381	064381			
AC	064381;			
DT	01-NOV-1996 (TREMBlrel. 01, Created)			
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)			
DT	01-NOV-1999 (TREMBlrel. 12, Last annotation update)			
DE	B7-2.			
GN	CD86 OR B7-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129;			
RX	BEDLINE: 96094437.			
RA	Mordello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;			
RT	"Differential expression of alternate mb7-2 transcripts.";			
RL	J. Immunol. 155:5490-5497(1995).			
DR	EMBL: U39456; AAC52333.1; -			
DR	EMBL: U39392; AAC52333.1; JOINED.			
DR	EMBL: U39457; AAC52333.1; JOINED.			
DR	EMBL: U39462; AAC52333.1; JOINED.			
DR	EMBL: U39463; AAC52333.1; JOINED.			
DR	EMBL: U39464; AAC52333.1; JOINED.			
DR	EMBL: U39465; AAC52333.1; JOINED.			
DR	EMBL: U39466; AAC52333.1; JOINED.			
DR	EMBL: U39456; AAC52333.1; -			
DR	EMBL: U39465; AAC52333.1; JOINED.			
DR	EMBL: U39466; AAC52333.1; JOINED.			
DR	EMBL: U39392; AAC52333.1; JOINED.			
DR	EMBL: U39457; AAC52333.1; JOINED.			
DR	EMBL: U39461; AAC52333.1; JOINED.			
DR	EMBL: U39462; AAC52333.1; JOINED.			
DR	EMBL: U39463; AAC52333.1; JOINED.			
DR	EMBL: U39464; AAC52333.1; JOINED.			
DR	EMBL: U39465; AAC52333.1; JOINED.			
DR	EMBL: U39466; AAC52333.1; JOINED.			
DR	EMBL: U39467; AAC52333.1; JOINED.			
DR	EMBL: U39468; AAC52333.1; JOINED.			
DR	EMBL: U39469; AAC52333.1; JOINED.			
DR	EMBL: U39470; AAC52333.1; JOINED.			
DR	EMBL: U39471; AAC52333.1; JOINED.			
DR	EMBL: U39472; AAC52333.1; JOINED.			
DR	EMBL: U39473; AAC52333.1; JOINED.			
DR	EMBL: U39474; AAC52333.1; JOINED.			
DR	EMBL: U39475; AAC52333.1; JOINED.			
DR	EMBL: U39476; AAC52333.1; JOINED.			
DR	EMBL: U39477; AAC52333.1; JOINED.			
DR	EMBL: U39478; AAC52333.1; JOINED.			
DR	EMBL: U39479; AAC52333.1; JOINED.			
DR	EMBL: U39480; AAC52333.1; JOINED.			
DR	EMBL: U39481; AAC52333.1; JOINED.			
DR	EMBL: U39482; AAC52333.1; JOINED.			
DR	EMBL: U39483; AAC52333.1; JOINED.			
DR	EMBL: U39484; AAC52333.1; JOINED.			
DR	EMBL: U39485; AAC52333.1; JOINED.			
DR	EMBL: U39486; AAC52333.1; JOINED.			
DR	EMBL: U39487; AAC52333.1; JOINED.			
DR	EMBL: U39488; AAC52333.1; JOINED.			
DR	EMBL: U39489; AAC52333.1; JOINED.			
DR	EMBL: U39490; AAC52333.1; JOINED.			
DR	EMBL: U39491; AAC52333.1; JOINED.			
DR	EMBL: U39492; AAC52333.1; JOINED.			
DR	EMBL: U39493; AAC52333.1; JOINED.			
DR	EMBL: U39494; AAC52333.1; JOINED.			
DR	EMBL: U39495; AAC52333.1; JOINED.			
DR	EMBL: U39496; AAC52333.1; JOINED.			
DR	EMBL: U39497; AAC52333.1; JOINED.			
DR	EMBL: U39498; AAC52333.1; JOINED.			
DR	EMBL: U39499; AAC52333.1; JOINED.			
DR	EMBL: U39500; AAC52333.1; JOINED.			
DR	EMBL: U39501; AAC52333.1; JOINED.			
DR	EMBL: U39502; AAC52333.1; JOINED.			
DR	EMBL: U39503; AAC52333.1; JOINED.			
DR	EMBL: U39504; AAC52333.1; JOINED.			
DR	EMBL: U39505; AAC523			

[illegible]

QY 304 PE 305
DB 342 KE 343

RESULT 7

035531 PRELIMINARY; PRT; 313 AA.
AC 035531.
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE MEMBRANE GLYCOPROTEIN PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR LEWIS (LEW/CRJ); TISSUE-LYMPHOMA;
RX MEDLINE; 97380318.
RA Maeda K., Sato T., Azuma M., Yagita H., Okumura K.;
RT "Characterization of rat CD80 and CD86 by molecular cloning and mab."
RL Int. Immunol. 9:993-1000(1997).
DR EMBL; D50558; BAA23470.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 1g; 1.
KW Signal; Membrane.
FT CHAIN 1 29 POTENTIAL.
FT SIGNAL 30 313 CD28 AND CTLA4 LIGAND.
SQ SEQUENCE 313 AA; 35573 MW; 3106246B8901B5D5 CRC64;

Query Match 40.5%; Score 702.5; DB 11; Length 313;
Best Local Similarity 55.0%; Pred. No. 2e-52;
Matches 148; Conservative 33; Mismatches 83; Indels 5; Gaps 3;

QY 5 CTMGSLILFYMAFLISGAAPLKIQAAYFNETADLPCOFANSQNSSELYVFWQDENVL 64
DB 10 CTMYGILFSLVAYLISAVVAVKQAFVNSAYVLPCEFTKAQNSPELVVFNQDKKVS 69
QY 65 LNEYVLGKEKDSVSKMGRTSPDSWTLRLNLQIKKGLKQCLIHKKKPTGMIRH 124
DB 70 LYEHVLGAEKLDNVAKYLGRTSPDRNQALRLHNVQIKDTGYDCFTQGTGSIID 129
QY 125 QMSSELVLANFSOPELPIISNTENYINLTCSHGYEPKMSVLTSTKSTIEYDG 184
DB 130 QMETELSIANFSPELEEAQNETRNGINLTCSKQGYKPTKMYFLI--TSTNEYGD 187
QY 165 IMQKQDQNTVELYDVYSISLSPFDVYSNMNIFILETDKTRLLSPFSIELEDPPQPP 244
DB 188 NMQISQDQNTKLFVSISLSPDPGVYNMNITVCILETSMNISKRPHNVFSQPO--PD 245
QY 245 HIPWITAVLPVLCVWFCLIMKMKKK 273
DB 246 RKTWQIAGPSSILCCL-FLVYVKKAYK 273

RESULT 8

062810 PRELIMINARY; PRT; 149 AA.
AC 062810.
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE B7-2 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Goodman R.E., Pastoriza L., Fak J.J., Toews G.B.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U31330; AAA74282.1; -.
FT NON_TER 1
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 17153 MW; A649D99DFEC42F11 CRC64;

Query Match 26.1%; Score 453; DB 11; Length 149;
Best Local Similarity 62.4%; Pred. No. 1.7e-31;
Matches 93; Conservative 15; Mismatches 39; Indels 2; Gaps 1;

QY 49 SLSELVFWQDENVLNEYLGKEKDSVSKMGRTSPDSWTLRLNLQIKDKGLY 108
DB 2 SLSELVFWQDKRSVLYEHLGAEKLDNVAKYLGRTSPDRNQALRLHNVQIKDTGY 61
QY 109 QCIHKKPPTGMIRHOMNSSELVLANFSOPELPIISNTENYINLTCSHGYEPK 168
DB 62 DCFIQKPTGISLQQWETELSIANFSPELEEAQNETRNGINLTCSKQGYKPTK 121
QY 169 MSVLTSTKSTIEYDGIMQKQDNTLEY 197
DB 122 MYFLI--TSTNEYGDNMQISQDNTLELF 148

RESULT 9

09R129 PRELIMINARY; PRT; 306 AA.
AC 09R129.
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE B LYMHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR.
GN CD80.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J; TISSUE-SPLEEN;
RA Ma R.Z., Teuscher C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065893; AAD25876.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 1g; 2.
SQ SEQUENCE 306 AA; 34531 MW; 1DB9EE3B6C1921F2 CRC64;

Query Match 14.0%; Score 243; DB 11; Length 306;
Best Local Similarity 27.9%; Pred. No. 4e-13;
Matches 89; Conservative 57; Mismatches 121; Indels 52; Gaps 16;

QY 12 ILFYMAFLISGAAPLKIQAAYFNETAD---LPCOFANSQNSSELYVFWQDENVLNEY 68
DB 23 LLPVILIRLSQVSSDVEQSKSVKDKVLLPCRY--NSPHEDESEDRITQKDKVYLS-V 80
QY 69 YLGKEKDSVSKMGRTSPDSWTLRLNLQIKKGLKQCLIHKKKPTGMIRI-HQMN 127
DB 81 TAGKLR--VPEYKKNRTLLDNTTYSLLILGLVLSDRGTSCV--OKKRGYEVKHAL 136
QY 128 SELVLANFSOPELPIISNTENYINLTCSHGYEPKMSVLTSTKSTIEY 182
DB 137 VKLSIKADESTPNITBSGNSAGTK--RITCFAGSGPCKP--RESWLENGRELPGIMTTI-- 192
QY 183 DGIQKQDQNTVELYDVYSISLSPFDVYSNMNIFILETDKTRLLSPFSIELEDPPQPP 242
DB 193 -----SQDPESELYTYSQIDP--NTRNHTIKCLITYGAH-VSEDFIWE-KPPDP 241
QY 243 PDHIPWIT-----AVLPVLCVWFCLIMKMKKKRRPNYSKCGTNTRESESEOT 295
DB 242 PDKNLTIVLFGAGGAVITVIVITIKKFC-----KHSKCF-----RNEASRE 286
QY 296 KKRKIHIPERSDEAKYVF 314

Db 287 TNSLTFCPEALAEQTVF 305

RESULT 10

ID	046405;	PRELIMINARY;	PRT;	296 AA.
AC	046405;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	CD80 ANTIGEN PRECURSOR (FRAGMENT).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
PN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Parsons K.R., Howard C.;			
RL	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: Y09950; CAA71081.1; -.			
DR	INTERPRO: IPR003006; -.			
DR	PFAM: PF00047; 1g; 2.			
KW	Signal.			
FT	SIGNAL.	1	25	POTENTIAL.
FT	NON_TER	296	296	
QC	SEQUENCE	296 AA;	33618 MM;	7ADB1IB5F532EF5 CRC64;

Query Match	13.3%;	Score 231;	DB 6;	Length 296;
Best Local Similarity	27.1%;	Pred. No. 4e-12;		
Matches 82;	Conservative 57;	Mismatches 122;	Indels 42;	Gaps 16;

```

QY 9 LSNILFV--MABLLSGAPLKIQAFNEMTADLPQOPANSQNSQSLSEVLVFWODDENLYLN 66
Db 19 LSGVLVLGLFPGFCGILTRKRVTKRVEIYMLSCDY--N7STBELSLKATIQMOKSKAVL- 76
QY 67 EYVLGKEKADSVHAKSYIMGRFSD--SDSWTRLHLNLOIKRKLXOCIIHHKKPTGIRIHO 125
Db 77 AILPGVVO--VMPYRKWRTITDMNDPRIVIALRLSDSGYTCVIOKPDLKGYKLEH 133
QY 126 MNS-ELSYLANFSQEIPIPISENITENYIMLTCSHIGYPEEK----KMSVLLRTKNSTI 180
Db 134 LTVSVRLMIRADRPVPTINDLGNPSNIR-RLICSTSGGPRPHILWMLNGBELNATNTTL 192
QY 181 EYNGIMQKQDNVTLIYXVSLSEVSPDYVTSNMNLTFCLE--TDKTRLLSPFSFIELEDP 239
Db 193 -----SQDEPTEMLYMISELD--NMTSMHSFLCVYKKGDLT--VSQTFWQESKP 239
QY 240 QPPEP-ILIPWITAVLP-----TVILICVAFCLILMKKKKKRPNRSYKQNTNMEES 292
Db 240 TFSANQHLTW-TIIPVSAFISYIYAVILTCLTGNMAAIRQRR-----NEVEMESC 292
QY 293 EQT 295
Db 293 SOS 295

```

RESULT	11
002758	
AC	PRELIMINARY:
ID	PRT: 292 AA.
NC	002758
DT	01-JUL-1997 (TREMBLrel. 04, Created)
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	T-CELL SPECIFIC SURFACE GLYCOPROTEIN B7-1.
OS	Felis silvestris catus (Cat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Hash S.M.;
RL	Thesis (1996), Texas A&M University, USA.
RR	EMBL; U57755; AAB53575.1; -.

```
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig, 1.
SQ SEQUENCE 292 AA; 33482 MW; 6F117E7852B7950F CRC64;
```

Query Match	12.9%	Score 224;	DB 6;	Length 292;
Best Local Similarity	27.7%	Pred. No. 1.6e-11;		
Matches	78;	Conservative	61;	Mismatches 103;
			Indels	40;
			Gaps	17;

```

0Y 12 ILVWVAFLLSGAAPKICIAFYENFETADJPCOFANSONOSISELYVWPODEMIVJNEVYL 71
0Y 24 MLASLEYFCSGI--IQVKKYEBEVAVLSCDY-NISTKELTEIRITVQKQDEWVL-AVMSG 79
Db 72 KEKFDVSHKWKGRSFSD-SDSWTLRLHNIQDKGLYOCIIHHKKPMTGRHOMNS-E 129
Db 80 KVG---VWRKYKRRFTFVTJTNHNSIVJMALRLSDNGKRYCII-QRIENGSRVXVHLTSVM 135
0Y 130 LSVLANFSOPELVISNTENVTNYINTLCSSIHGPEPKMSVY-----LRRKNSFTIEDG 184
Db 136 LVRADFPVPSTIDLGANSHNIK-RIMCLTSGGFPKP-HLSWLENDEELMINTVY----- 189
Db 185 IMKSDONVETELYDVISLSVSPDVTSNMRTFCILETDKTRLLSSPRLSEIDPOPPD 244
0Y 190 -----SODPELEYLTISSEIDF---NMTRNNHSTFLCYKGNL-LVSOIFNMOKSEPOSSNN 241
Db 245 HIPPIATVLPVVICWV-----CII---LWKKKKKKR 277
0Y 242 QL-WI--ILLSVYSGIVITATLRLCYLHRRPAARMQREBGR 281

```

RESULT	12			
ID	055202	PRELIMINARY;	PRT;	321 AA.
AC	055202;			
DT	01-JUN-1998 (TREMBLrel. 06.	Created)		
DT	01-JUN-1998 (TREMBLrel. 06.	Last sequence update)		
DT	01-MAY-2000 (TREMBLrel. 13.	Last annotation update)		
DE	CS80.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-LEWIS ;			
RA	Sato T.; Azuma M.; Yagita H.; Okumura K.;			
RL	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-LEWIS ;			
RA	Maeda K.;			
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: U88622; AAC02262.1; -.			
DR	INTERPRO: IPR003006; -.			
PFAM: PF00447; 19; 2.				
SEQUENCE	321 AA; 36297 MW; 07ESB56E58BED6AF CRC64;			

		12.8%	Score 222;	DB 11;	Length 321;
Query Match		26.5%	Prod. No. 2	6e-11;	
Best Local Similarity		55;	Mismatches 115;	Indels 60;	Gaps
Matches	83;	Conservative			
OY	12	ILFVMAFLLSGAPAKLQAYFNETADLPCCF-ANSONQSLSELVYFMQDOENLYLNEYTL	70		
Db	27	LLVVLGFQJSTGIVGVGSKSVKREKALLSCDYKLCSEBQSJHRL-YWQKHBMVLSYL--	82		
OY	71	GKEKFDVSASHKMGKGRISPD-SDSVTLRLHLNQLDKDKGLQCIILHHKRPKMGKRIKHOMKSE	1229		
Db	83	--SGVPEWMEPEXKNRTVYDIANNYSFSLGLILSDRETYCVRQRYEGSGVYVYKHLATPVE	140		
OY	130	LSVLANSOPEIYIPISNTENYINLTNCSSIHGPGKSKSYL-----LFRKNSITIEDG	1844		
Db	141	LSVRADFPPIPNITESGNBPADK-RITCFASGGFPKP-RISMLENGRELNGINTTI-----	1944		


```
FT CONFLICT 33 33 F -> L (IN REF. 2).
FT CONFLICT 91 91 E -> K (IN REF. 2).
FT CONFLICT 155 155 S -> Y (IN REF. 2).
FT CONFLICT 213 213 T -> A (IN REF. 2).
FT CONFLICT 237 237 E -> V (IN REF. 2).
FT CONFLICT 250 250 I -> V (IN REF. 2).
FT CONFLICT 257 257 S -> P (IN REF. 2).
FT NON_TER 290 290
SQ SEQUENCE 290 AA: 32691 MW: 479A4B83EF0937C9 CRC64;
```

Query Match

12.2%; Score 211; DB 11; Length 290;

Best Local Similarity 26.3%; Pred. No. 2e-10; Mismatches 108; Indels 48; Gaps 14;

Matches 74; Conservative 51; Mismatches 108; Indels 48; Gaps 14;

```
QY 12 ILFVMAFLLSGAAPLKIQAYFNFETADLPQCPA-NSQNSLSSELYVFWQDQENLVINEVYL 70
DB 27 LLLVGLFQISSGIVGOVSKSVREKALLSCDYKFCSEQSIHR--IYQKHDKMVLSTV--- 82
QY 71 GKKEPDSVHSHKYMGRTPFD-SDSWTLRLHNLQIKDKGLYQCIHHKKPTGMIRIHQMNSE 129
DB 83 --SGVPEVWMEYKNNRYDIANNYSFSLGLILSDRGTYTCVQYREGGSYVVKHLTYE 140
QY 130 LSYLANFSOPEIYVPSNITENVTINLTCSIHGYPPPKKMSVL-----LRTKSTIEYDG 184
DB 141 LSYRADFPPTNITESGNPSADIK-RITCFASGGEPKP-RLSWLENGRELNGINTTI---- 194
QY 185 IMQKSDONTVELYDVSTISVSFPDVTSMNTIFCILETOKTRLLSSPFSIELEDPOPPD 244
DB 195 ----SDDPESELTYTISQLDLFT---NTTYDHFIDCFIEYGDAN-VSQNFTWE-KPPEDPPD 245
QY 245 H---IP--W-----ITAVLPVYIICVWVFCL 265
DB 246 EKOTIPFAMAGSDAVKAIIFFTAIATVIAIAIAIIFIICI 286
```

Search completed: November 6, 2000, 01:45:59
Job time: 2406 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2000, 00:41:07 ; Search time 649.78 Seconds
(without alignments)
32.132 Million cell updates/sec

Title: US-09-206-132-2

Perfect score: 1733
Sequence: 1 MDPOCTMGISNITLFVMAFL.....AQRVFKSKRTSCDSKSDTCE 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_65: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	100.0	329	1 A48754	B7-2 antigen - hum
2	963.5	55.6	330	2 I46691	CD86 precursor - r
3	743.5	42.9	309	2 I49522	gene B7-2 protein
4	243	14.0	299	2 I46690	CD80 precursor
5	243	14.0	309	2 I49503	B-lymphocyte activ
6	222	12.8	321	2 I54766	B-cell-restricted
7	201.5	11.6	288	2 A45803	B7 protein - red-c
8	187.5	10.8	289	2 G00031	butyrophilin - mou
9	173.5	10.0	487	2 S65133	butyrophilin - mou
10	167	9.6	526	2 S70587	butyrophilin - bo
11	162	9.3	526	2 A37821	tracitin - medica
12	131.5	7.6	1880	2 T18531	Ig lambda-like cha
13	129.5	7.5	238	2 A46633	OX-2 membrane gly
14	128	7.4	274	2 A47639	OX-2 membrane gly
15	128	7.4	278	1 TDRTOX	T cell activation
16	124	7.2	569	2 A46462	cell surface glyco
17	119.5	6.9	646	2 I18049	butyrophilin homol
18	118.5	6.8	391	2 T09058	leukocyte surface
19	113	6.5	1021	2 I39207	Ig heavy chain pre
20	112.5	6.5	549	2 S04845	c-mer tyrosine kin
21	110.5	6.4	994	2 I49276	Ig kappa chain - s
22	109.5	6.3	230	2 S33161	neurotrophin - rat
23	108.5	6.3	344	2 I56551	leukocyte antigen
24	106	6.1	243	2 A53244	signaling lymphoc
25	105	6.0	335	2 S58892	hypothetical prote
26	104.5	6.0	5175	2 T20992	hemocentin precus
27	104.5	6.0	5198	2 T43290	hypothetical prote
28	104	6.0	292	2 T44230	protein-tyrosine k
29	103	5.9	871	1 I48696	

30	103	5.9	881	1 I48697	protein-tyrosine k
31	102	5.9	931	2 T39143	hypothetical prote
32	101.5	5.9	739	2 S18642	polynucleotide ade
33	101.5	5.9	784	2 T18452	hypothetical prote
34	101	5.8	167	2 T19084	hypothetical prote
35	101	5.8	1274	2 I40813	neurotoxin type F
36	100.5	5.8	416	2 A54017	colon carcinoma-as
37	99	5.7	570	2 A57535	intrileukin 1 recep
38	98.5	5.7	941	1 TVMYMD	protein-tyrosine k
39	98	5.7	588	2 A45254	surface glycoprote
40	98	5.7	664	2 T50316	hypothetical Armad
41	97.5	5.6	285	2 S36903	FC gamma (IgG) rec
42	97.5	5.6	814	1 A39752	fibroblast growth
43	97.5	5.6	978	2 S16385	macrophage colony-
44	97	5.6	315	1 HNVZVT	hemagglutinin prec
45	97	5.6	392	1 RWH0PD	poliovirus recepto

ALIGNMENTS

RESULT 1

A48754

B7-2 antigen - human

N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A48754; S39055

R:Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard

Science 262, 909-911, 1993

A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr

A:Reference number: A48754; MUID:94053735

A:Accession: A48754

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-329 <FREE>

A:Cross-references: GB:125259; NID:q416368; PIDN:AA58389.1; PID:q416369

A>Note: It is uncertain whether Met-1 or Met-7 is the initiator

R:Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza,

Nature 366, 76-79, 1993

A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.

A:Reference number: S39055; MUID:94050123

A:Accession: S39055

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 7-329 <AZU>

A:Cross-references: GB:U04343; NID:q439838; PIDN:AA03814.1; PID:q439839

C:Genetics: A:Gene: GDB:CD86; CD28LG2

A:Cross-references: GDB:433597; OMIM:601020

A:Map position: 3q13.3-3q21

C:Superfamily: B7-2 antigen

C:Keywords: glycoprotein

Query Match 100.0%; Score 1733; DB 1; Length 329;
Best local similarity 100.0%; Pred. No. 3, 9e-121;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDPOCTMGISNITLFVMAFLGSAAPLKTOAFNEFADIPCOFANSONSLSLVVFMDD	60
DB	1	MDPOCTMGISNITLFVMAFLGSAAPLKTOAFNEFADIPCOFANSONSLSLVVFMDD	60
QY	61	EMLVNEVYLKKEKPDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLVQCIIHHKKPTGM	120
DB	61	EMLVNEVYLKKEKPDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLVQCIIHHKKPTGM	120
QY	121	IRIHOMNSLSVLANFSOPEIVPISNTEYINLTGSSIHGYEPKMSVLTTRKSTI	180
DB	121	IRIHOMNSLSVLANFSOPEIVPISNTEYINLTGSSIHGYEPKMSVLTTRKSTI	180
QY	181	EVDGIMOKSODNVTETLYDVISLSVSPDYNSNMFTFCILEFDKRLISPFSTLEDDPQ	240
DB	181	EVDGIMOKSODNVTETLYDVISLSVSPDYNSNMFTFCILEFDKRLISPFSTLEDDPQ	240

```

Db      181 EVDGIHQKQDQVNTELYDVISISVSFDPVTSNMTIFCLLEFDKTRLLSSPFSIELEDPQ 240
QY      241 PPPDHPWITATLAPVYITCVMPFCLILMKKKKKRPNRSYKCGTNTMEREESEQTKRK 300
        |||
Db      241 PPPDHPWITATLAPVYITCVMPFCLILMKKKKKRPNRSYKCGTNTMEREESEQTKRK 300
QY      301 IHIPERDEAORVRFKSSKTSKCDKSDTCP 329
        |||
Db      301 IHIPERDEAORVRFKSSKTSKCDKSDTCP 329
        |||

RESULT  2
146691
CD86 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46691
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849
A:Accession: I46691
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-330 <ISO>
A:Cross-references: GB:D49842; NID:g755098; PIDN:BA08642.1; PID:g755099
C:Superfamily: B7-2 antigen

```

Query Match	55.6%	Score 963.5;	DB 2;	Length 330;
Best Local Similarity	58.0%	Pred. No. 3.6e 64;		
Matches 192; Conservative	52;	Mismatches 84;	Indels 3;	Gaps 3;

QY	1	MDPOCTMGISNLTSEFMAFLTSGAAPLKTOAYENENADLPCCOFRANSQNSQSLSELYWYWDQ	60
Db	1	MDAGCTMGISYVFEFMAFLTSGAASLRIOAYFNKTRADLPCCOFTNNSQSLSELYWYWDQ	60
QY	61	ENLVINEVYLCKEKFDSVSHKYMGRTSEFSDSWTLRLNHIQTRDKGLXOYCIITHKKKPTGM	120
Db	61	ERLVYELTEFLFKREKPDNDVPKTYIGRTSEFQESMNLTQHNWQIKDKGVYQCFVHHNGRGL	120
QY	121	IRIHQMSSELVIANFSQPEIVPISNITENYVINTCSSIHQYPRPKKMSVYLTRKNSIT	180
Db	121	VPIQMSSELVIANFTQPEITILISNITRNSAINITCSSVQGIPEPKKMFVFKLTENATF	180
QY	181	EYDGIQMSQDNVTLEYVVISLSVSPDYVTSNMFTFCILETDKTRLLSSPSISIELEDP	240
Db	181	EYDGVIEISQDNVTGLYINISISGSIETFSODIDRNATYCVLQTESIETYSQHPPIVADPV	240
QY	241	PPPHIPIPIITAV-LPTVITICVWFCLILMKMKKKRRPNRSYSCGNTMRESEQTKKE	299
Db	241	PVEKPRILMAIVALLTLYVCGIVLEFLTMKKRKEQDP-GVCECEITIKMDKAEHVEERY	299
QY	300	KIHPIER-SDEAQRVFKSKTSSCDKSDPTCF	329
Db	300	KIHPEKIPAKAACCEHRLKTPSSDSAAHF	330

```

RESULT      3
149522
gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: 149522
R:Premman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J. Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell pro
A:Reference number: 149522; MUID:94065585
A:Accession: 149522
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:I25606; NID:g432478; PIDN:AAA79770.1; PID:g432479

```

C;Genetics:
A;Gene: B7-2
C;Superfamily: B7-2 antigen

Query Match	42.9%;	Score	743.5;	DB	2;	Length	309;
Best Local Similarity	51.5%;	Pred.	No. 6.4e-48;				
Matches	158;	Conservative	45;	Mismatches	91;	Indels	13;
						Gaps	5;

QY	1	MDPOCTMELSNITLVYMFNFLLSGAPLKTQAFNFETADLPQOFANSONOSISELVTWQDQ	60
Db	1	MDPCKTMBGLATLLIETVYLLIDDAVSVEIOAFNFGTALPCKPFTKQAQNISSELTWVWQDQ	60
QY	61	ENLVNLEVYLKERKFDVSHSKYMGRTSFSDSWTLRLHNLQIDKGLQYCCIHHKRPFGM	120
Db	61	OKLVYEHYHLESTEKLDSDVNAKYLTGRTSEFDRNNMTLRLHNVQIKDMGSDYCFQKPKPTGS	120
QY	121	IRIHOMNSELVLNFSOPETVPIISNTTEWVYINLTGSSIHGVPBPKKMSVLLRTKNSIT	180
Db	121	IIIQOITLTELVSIVNFSEPELTKLAQNVTAQNGSINLTCTSKQGHKPKKMFEL--TNSTN	178
QY	181	EYDGIWMQSDQNVTELYDVSISLVSFSPDYTSNMTIFCLIDETKTRLLSPFSFTELEDQ	240
Db	179	EYGNMQISQDQNVTELETSISLSSLSFDPDVMMHTVAVCYLETESMKISSKPLNFQEPSS	238
QY	241	PPPDHIFP--LTAVLPPVVICVWFCLILMKKKKKRRPRNSYKCGINTMRESBQTKRR	298
Db	239	P---QTYMKETLTSVYVALLVHML--LIIYCHKKKPNQPSRP---SWTASKLERDSNADR	289
QY	299	EKIHIPE 305	
Db	290	ETINLEKE 296	

RESULT 4
I46690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: I46689; MUID:95369849
A:Accession: I46690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:g755096; PIDN:BA08643.1; PID:g755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match	14.0%	Score 243;	DB 2;	Length 299;
Best Local Similarity	25.8%	Pred. No. 7e+11;		
Matches 81; Conservative	65;	Mismatches 122;	Indels 46;	Gaps 14;

[illegible]

Db 234 KQEPIDQLFVW--IIFVSGALVLTAVVLCXCLACRAVAMKRRRR-----N 278
 Oy 290 EESQTKKREKIHT 303
 Db 279 EEFVGTERTLSPIYL 292
 RESULT 5
 149503
 B-lymphocyte activation antigen 7 precursor - mouse
 N:Alternate names: MB7-2
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequenceRevision 02-Jul-1996 #textChange 29-Sep-1999
 C:Accession: I49503; S17291; I49521
 R:Selvakumar, A.; White, P.C.; Dupont, B.
 Immunogenetics 38, 292-295, 1993
 A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
 A:Reference number: I49503; MUID:93307789
 A:Accession: I49503
 A:Status: preliminary; translated from GB/EMBL/DBDJB
 A:Molecule type: DNA
 A:Residues: 1-309 <RES>
 A:Cross-references: GB:L12589; NID:g293299; PIDN:AAA37240.1; PID:g293301
 R:Fireman, G.J.; Gray, G.S.; Gimmli, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fingerot
 J. Exp. Med. 174, 625-631, 1991
 A:Title: Structure, expression, and T cell costimulatory activity of the murine homologue
 A:Reference number: S17291; MUID:91341422
 A:Accession: S17291
 A:Molecule type: mRNA
 A:Residues: 1-274,'R', 279-309 <RE>
 A:Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
 R:Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.
 Biochem. Biophys. Res. Commun. 200, 443-449, 1994
 A:Title: Identification of an alternatively spliced form of the murine homologue of B7.
 A:Reference number: I49521; MUID:94220123
 A:Accession: I49521
 A:Status: translated from GB/EMBL/DBDJB
 A:Molecule type: mRNA
 A:Residues: 1-143,238-274,'R', 279-309 <RE2>
 A:Cross-references: GB:D16220; NID:g505118; PIDN:BA03748.1; PID:g994769
 C:Genetics:
 A:Gene: B7
 A:Introns: 37/1; 143/1; 237/1; 275/1
 C:Superfamily: B-lymphocyte restricted antigen B7
 C:Keywords: alternative splicing
 Query Match 14.0%; Score 243; DB 2; Length 309;
 Best Local Similarity 29.8%; Pred. No.7,3e-11;
 Matches 91; Conservative 53; Mismatches 119; Indels 42; Gaps 16;
 Oy 12 LTFVNAFLSGAAPRIQAYFNETAD--LPCOFANSQMSISELVYFMODENLVANEY 68
 Db 23 LTFVLLIRLSQVSDVDEQLSKSVKDKVLLPCRY-NSPHDESEDRIVQKHDKVLS-V 80
 Oy 69 YLCKEKFDVSHSKYMGRTSPDSQWFLRLHNLQIKDKGYOCIIHHKPKFGMIRI-HQNM 127
 Db 81 IACKLR---VWPEYKRNRLTDNNTYSLLIIGLVLSRGYISCVY-OKKRGTEYVAKHL 136
 Oy 128 SELSVANFSEOPETIVISNTENVYINLCCSHIGYPEPKMSVL-----LRTKSTIEY 182
 Db 137 VKLSIKADFTSPITFSGNSADTK-RITCFASGCPKP-RFSMLNNGRELPIGINTTI-- 192
 Oy 183 DGIKMSQDNVETELDVYSISLSVFPDYNSNMIFLCILEDKTRLLSPSILEDPOPP 242
 Db 193 -----SQDESELYTISQIDP--NTTKRHITKILIKIGDAH-VSEDTWE-KPEDP 241
 Oy 243 PDHLPWIT-----ALPFIIVICVWFCLILKKWKKRRKRSYKGTN---TMEEE- 291
 Db 242 PDKNTLVLFAGAGGANITVAVIIVIIKCFCKHNLAGSCPRRDEASRETNNSLTFGEPA 301
 Oy 292 -SEQT 295

RESULT 6
154766 B-lymphocyte activation antigen 7-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
A:Accession: I54766
R:Jung, T.A.; Lu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Intc. Immunol. 7, 171-178, 1995
A>Title: Cloning the rat homolog of the CD28/CtLA-4 ligand B7-1: structural and funct
A:Reference number: I54766; MUID:95252184
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-321 <RES>
A:Cross-references: EMBL:U05593; NID:g453381; PIDN:AAA80154.1; PID:g453382
C:Superfamily: B-Lymphocyte restricted antigen B7

Query Match 12.8%; Score 222; DB 2; Length 321;
Best Local Similarity 25.5%, Pred. No. 2,7e-09;
Matches 83; Conservative 59; Mismatches 116; Indels 68; Gaps 17;

OY 7 MGSLNLEPMARFLSGAAPLKIAQ-----YNENPADLPCCRA-NSQNLSSELVFEW 57
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 14 LGFPRIRFIHLFVLILLGLDITSSGIVGVAKSVREKALLSCDKFCSEDSIHR--ITY 71
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 58 QDOENVLYNEGYLGKEKFDSDYSKYMGRTSPD-SDSWTLRLHNLQIKDKGLYCIIHHKK 116
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 72 QKHDKMQLSVI---SGPEVEWPATKNTTYVDIANNTSFSLIGLLSDRGHTYICVGRYE 127
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 117 PTGMIRIHOMNELSYLANFSQPETIPISNTENYINLTCSIHGIPEPKMSYL---- 172
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 128 GGSYYVKHLITVELSIRADFPPTNITEYGNGPSADIK-RITFASGGEPKP-RLSMLENGR 185
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 173 -LRTKSTIEYOGIMOKSQDNATELYDVYSISVSFFPVTSMNMTFCLLETDRKLRLSSP 231
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 186 ELINGIMTTL-----SDDPESELTITSSQLDF---NATDHPLDCIEFGDGH-VSQN 233
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 232 FSILEDDPOPPDH---IP-W-----ITAVLPVIICVMFCLILMKWK 271
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 234 FT-WVRPEDPDPEKOTVFPMAGPDVAVKALITFIATLVIAVIAAIILIFCITV-KFR 291
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 272 KKRPRNSYKCGTNMERESBOTKK 297
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 292 RCRRRN-----EASRETNR 306
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 7
A45803 B-cell-restricted antigen B7 precursor - human
N:Alternate names: B-Lymphocyte activation antigen B7
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
A:Accession: I54495; A45803
R:Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
Immunogenetics 36, 175-181, 1992
A>Title: Genomic organization and chromosomal location of the human gene encoding the
A:Reference number: I54495; MUID:92307753
A:Accession: I54495
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-286 <RES>
A:Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329
R:Freedman, G.J.; Freedman, A.S.; Segill, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.
J. Immunol. 143, 2714-2722, 1989
A>Title: B7, a new member of the Ig superfamily with unique expression on activated a
A:Reference number: A45803; MUID:90010147
A:Accession: A45803
A:Molecule type: mRNA

C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 7.5%; Score 129.5; DB 2; Length 238;
Best Local Similarity 23.0%; Pred. No. 0.013;
Matches 53; Conservative 52; Mismatches 99; Indels 33; Gaps 11;
QY 12 ILFWAFLLSG-----AAFLKIQAYFNETADLPQFANSONOSISELVFWMQDE-- 61
DB 7 LIMPLAFVAGISGDIWTFQSPVLSVGLQGTATITC-----TASQSIYSNLAMYQQRREG 62
QY 62 --NLVNLVYLGKEKFDVSHKYMGRTSFSDSWTLRLHNLQIKDKGLYCCIIHKKPTG 119
DB 63 KPSSL--IYATNRKTYGVSERFSG--SGSQTFTLTISVWQEDVADYCCQAYGSYSQ 117
QY 120 MIRIHMNSSEVLANFSQPEIPIVPSNITENVY----INLCSSIHGYPEPKMSVLLRT 175
DB 118 RLAFPK-GTKRLSRSDRSQPKLTLLPSPDQVQTKGATLVCILANHPPELQVQ--WK 173
QY 176 KNSTIEYGIQKSDQNTVE-LYDVSISLSVSPDVTSMNTTICILETDKTRLLSPFS 233
DB 174 KDGAIVSDGVQTSNLRASDSTYSVSLTLTSGSDWESNARFSCAL-THTV--LSSPLS 229

RESULT 14

A:47639

OX-2 membrane glycoprotein precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence.revision 31-Dec-1993 #text.change 20-Jun-2000

C:Accession: A47639

R:McCaughan, G.W.; Clark, M.J.; Barclay, A.N.

Immunogenetics 25, 329-335, 1987

A:Title: Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein

A:Reference number: A47639; MUID:87192943

A:Accession: A47639

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-274 <MCC>

A:Cross-references: GB:X05323; NID:934742; PIDN:CAA28943.1; PID:g1335216; GB:M17226; GB:

C:Superfamily: MRC OX-2 antigen; immunoglobulin homology

C:Keywords: glycoprotein; membrane protein

F:40-119/Domain: immunoglobulin homology <IMM>

Query Match 7.4%; Score 128; DB 2; Length 274;

Best Local Similarity 21.1%; Pred. No. 0.02;

Matches 63; Conservative 57; Mismatches 120; Indels 58; Gaps 16;

QY 11 NILFWAFLLSGAAPLKI-----QAVFNETADLPQFANSONOSISELVFWMQD--- 60
DB 13 SLVWMAVAIVCTAQOVVYQDERDYL--TTASLKCSLQNAQ---EALITVWQKKAV 66
QY 61 --ENLVL-----NEVYLGKEKFDVSHKYMGRTSFSDSWTLRLHNLQIKDKGLYCCIIH 114
DB 67 SPENNVTSEHNGVYIQAYKDKINIQGLQNSTITFW-----NITLDEGCYMCLEFN 120
QY 115 KKPFGMIRIHMNSSEVLANFSQPEIPIVPSNITENVYINLTGSSIHGYPEPKMSVLLR 174
DB 121 --TFEGFKI---SGTACLTIVYQV--IVSLHYKFESEDLNITCSAT--ARPA--WVFWK 169
QY 175 TKNSTIEYGIQKSDQNTVE-LYDVSISLSVSPDVTSMNTTICILETDKTRLLS 229
DB 170 VPRSGIENSTVTLSPHNTTSVTSI---LHKDPKNQGVKEVICQVHLGTVDTFQQTVA 226
QY 230 SPFSIELEDDPPDPDHPWITAVLPYIICVWFCLIMKKKKKKRPRNSYKCGTNTM 287
DB 227 KGYWFS-----VPLLSTIVSLVLLVLSILLYMK--RRHNDRGELSGQVQKM 273

RESULT 15

TDRKX

OX-2 membrane glycoprotein precursor - rat

N:Alternate names: MRC OX-2 antigen
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Dec-1986 #sequence.revision 04-Dec-1986 #text.change 22-Jun-1999

C:Accession: A02114

R:Clark, M.J.; Gagnon, J.; Williams, A.F.; Barclay, A.N.

EMBO J. 4, 113-118, 1985

A:Title: MRC OX-2 antigen: a lymphoid/neuronal membrane glycoprotein with a structure

A:Reference number: A02114; MUID:85257428

A:Accession: A02114

A:Molecule type: mRNA

A:Residues: 1-278 <CLA>

A:Cross-references: GB:X01785; NID:956700; PIDN:CAA25925.1; PID:956701

C:Comment: This protein is found on the surface of neurons, thymocytes, B cells, and

C:Superfamily: MRC OX-2 antigen; immunoglobulin homology

C:Keywords: glycoprotein; surface antigen; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <Sig>

F:31-278/Product: OX-2 membrane glycoprotein #status predicted <IMM>

F:44-123/Domain: immunoglobulin homology <IMM>

F:153-229/Domain: immunoglobulin homology <IMM>

F:233-259/Domain: transmembrane #status predicted <TM>

F:260-278/Domain: intracellular #status predicted <INT>

F:51-121,160-214/Disulfide bonds: #status predicted

F:95,103,110,157,181,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.4%; Score 128; DB 1; Length 278;

Best Local Similarity 22.1%; Pred. No. 0.021;

Matches 70; Conservative 53; Mismatches 128; Indels 66; Gaps 16;

QY 3 POCWTGSLNILEFWAFLLSGAAPLKI-----QAVFNETADLPQFANSONOSISELVFW 57
DB 9 PCHLSSTSLMAIAVAALSTAGVEVYQDERDYLTTASLKCSLQNTA---EPLITVW 64
QY 58 QDO-----ENLVL-----LNEVYLGKEKFDVSHKYMGRTSFSDSWTLRLHNLQIKDKGLY 108
DB 65 OKKRAVGPENNVYTSKAGVYQPTKYKDRINTELGLNSTITFW-----NTLDEGCY 119
QY 109 OCIIHKKPTGMIRIHMNSSEVLANFSQPEIPIVPSNITENVYINLTGSSIHGYPEPK 168
DB 120 MCLF-NMEGSGKV-----SGTACLTIVYQPIVHLHNYFED--HLNITCSAT--ARPA-- 168
QY 169 MSVLLRTNKTIEYGIQKSDQNTVE-LYDVSISLSVSPDVTSMNTTICILETDKTRLLS 223
DB 169 -AISWKGTSGLF--NSTESHSHNGTT--SVSTILRYKDKTQVQGEVICOVLYLGAVTD 224
QY 224 KTRLLSPFSIELEDDPPDPDHPWITAVLPYIICVWFCLIMKKKKKKRPRNSYKCG 283
DB 225 YKQSLDKGFWS-----VPLLSTIVSLVLLVLSILLYMK-----KRHN----- 264
QY 284 TMTMRESEBQTKRK 300
DB 265 ---QERGESSQGMQRMK 278

Search completed: November 6, 2000, 01:27:53
Job time: 2806 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 5, 2000, 23:47:27 ; Search time 239.95 Seconds
(without alignments)
22.982 Million cell updates/sec

Title: US-09-206-132-2

Perfect score: 1733
Sequence: 1 MDPOCTMGLSNILFVMAFL.....AQRVFKSKTSSCDKSDTCF 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 segs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1733	100.0	329	2	US-08-456-104-2
2	1733	100.0	329	2	US-08-101-624-2
3	1733	100.0	329	3	US-08-479-744A-2
4	1733	100.0	329	4	PCT-US95-02576-23
5	1696	97.9	323	4	PCT-US94-09642-2
6	743.5	42.9	309	3	US-08-456-104-4
7	743.5	42.9	309	3	US-08-479-744A-23
8	743.5	42.9	309	4	PCT-US95-02576-21
9	724.5	41.8	314	4	PCT-US95-02576-13
10	577	33.3	110	3	US-08-479-744A-45
11	517	29.8	102	3	US-08-479-744A-47
12	328	18.9	61	4	PCT-US95-02576-32
13	245.5	14.2	320	4	PCT-US95-02576-2
14	244	14.1	306	4	PCT-US95-02576-17
15	242	14.0	306	2	US-08-147-772-4
16	242	14.0	306	2	US-08-456-104-8
17	242	14.0	306	2	US-08-101-624-25
18	242	14.0	306	2	US-08-153-262-4
19	242	14.0	306	3	US-08-479-744A-21
20	201.5	11.6	288	2	US-08-147-772-2
21	201.5	11.6	288	2	US-08-456-104-6
22	201.5	11.6	288	2	US-08-101-624-23
23	201.5	11.6	288	2	US-08-751-767A-6
24	201.5	11.6	288	3	US-08-153-262-2
25	201.5	11.6	288	3	US-08-479-744A-29
26	201.5	11.6	288	4	PCT-US95-02576-19
27	185	10.7	208	4	US-08-630-172-15
28	160.5	9.3	610	2	US-08-724-394A-5

29	159	9.2	342	2	US-08-724-394A-6	Sequence 6, Appl
30	157	9.1	540	2	US-08-724-394A-4	Sequence 4, Appl
31	150	8.7	589	2	US-08-724-394A-1	Sequence 1, Appl
32	132	7.6	212	4	PCT-US95-02576-63	Sequence 63, Appl
33	132	7.6	226	4	PCT-US95-02576-65	Sequence 65, Appl
34	128.5	7.4	200	4	PCT-US95-02576-9	Sequence 9, Appl
35	126.5	7.3	581	2	US-08-724-394A-2	Sequence 2, Appl
36	124	7.2	214	4	PCT-US95-02576-11	Sequence 11, Appl
37	121.5	7.0	581	2	US-08-724-394A-3	Sequence 3, Appl
38	118.5	6.8	365	2	US-08-979-424-3	Sequence 3, Appl
39	107	6.2	242	1	US-08-398-613A-56	Sequence 56, Appl
40	107	6.2	242	1	US-08-398-612A-56	Sequence 56, Appl
41	107	6.2	242	1	US-08-398-611A-56	Sequence 56, Appl
42	107	6.2	242	2	US-08-491-334A-56	Sequence 56, Appl
43	107	6.2	242	3	US-09-027-449-42	Sequence 42, Appl
44	107	6.2	242	3	US-08-804-444A-42	Sequence 42, Appl
45	106.5	6.1	393	1	US-08-429-742-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-456-104-2
Sequence 2, Appl 104-2
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-2

Query Match 100.0%; Score 1733; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPCGTGSLNILEFVNAFLISGAAPLKIOAYENETADLPQOFANSQNSLSLVLVFWMDQ 60
DB 1 MDPCGTGSLNILEFVNAFLISGAAPLKIOAYENETADLPQOFANSQNSLSLVLVFWMDQ 60
QY 61 ENLVNENYVIGKEKPEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVNENYVIGKEKPEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
QY 121 IRIHONNSELVLANFSOPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
DB 121 IRIHONNSELVLANFSOPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
QY 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCILETDKTRLLSSPFSIELEDPQ 240
DB 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCILETDKTRLLSSPFSIELEDPQ 240
QY 241 PPDPHIMWITAVLPTVILICMVFCILIMKKKKRRPRNSYKCGTNTMERESBOTKKREK 300
DB 241 PPDPHIMWITAVLPTVILICMVFCILIMKKKKRRPRNSYKCGTNTMERESBOTKKREK 300
QY 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329
DB 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329

RESULT 2

US-08-101-624-2
Sequence 2, Application US/08101624
Patent No. 5942607
GENERAL INFORMATION
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 ligands and
TITLE OF INVENTION: Uses therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-101-624-2

Query Match 100.0%; Score 1733; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 2,4e-154;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPCGTGSLNILEFVNAFLISGAAPLKIOAYENETADLPQOFANSQNSLSLVLVFWMDQ 60
DB 1 MDPCGTGSLNILEFVNAFLISGAAPLKIOAYENETADLPQOFANSQNSLSLVLVFWMDQ 60
QY 61 ENLVNENYVIGKEKPEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVNENYVIGKEKPEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
QY 121 IRIHONNSELVLANFSOPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
DB 121 IRIHONNSELVLANFSOPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
QY 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCILETDKTRLLSSPFSIELEDPQ 240
DB 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCILETDKTRLLSSPFSIELEDPQ 240
QY 241 PPDPHIMWITAVLPTVILICMVFCILIMKKKKRRPRNSYKCGTNTMERESBOTKKREK 300
DB 241 PPDPHIMWITAVLPTVILICMVFCILIMKKKKRRPRNSYKCGTNTMERESBOTKKREK 300
QY 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329
DB 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329

RESULT 3

US-08-479-744A-2
Sequence 2, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
TITLE OF INVENTION: Uses therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-744A-2

Query Match 100.0%; Score 1733; DB 3; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPQCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQFANSQNSQSLSELYVFWQDQ 60
DB 1 MDPQCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQFANSQNSQSLSELYVFWQDQ 60
QY 61 ENLYAVNEVYLGKREKFDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYQCIIHKKKPTGM 120
DB 61 ENLYAVNEVYLGKREKFDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYQCIIHKKKPTGM 120
QY 121 IRIHQMSSELYLANFQPEIIVPISNTENYINLTCSIHGYPEPKKMSVLLRTKNSI 180
DB 121 IRIHQMSSELYLANFQPEIIVPISNTENYINLTCSIHGYPEPKKMSVLLRTKNSI 180
QY 181 EYDGIQMSQDNVTELYDVSTISLSVSPDYTSNMRTFCLILETDKTRLLSPFSIELEDQ 240
DB 181 EYDGIQMSQDNVTELYDVSTISLSVSPDYTSNMRTFCLILETDKTRLLSPFSIELEDQ 240
QY 241 PPPDHIMTITAVLPTVIICVAVFCLILMKKKRRPRNSYKCGTNTMERESQTKKREK 300
DB 241 PPPDHIMTITAVLPTVIICVAVFCLILMKKKRRPRNSYKCGTNTMERESQTKKREK 300
QY 301 IHIPERSDEAQRVFKSSKTSKCDKSDTCF 329
DB 301 IHIPERSDEAQRVFKSSKTSKCDKSDTCF 329

RESULT 4
PCT-US95-02576-23
Sequence 23, Application PC/TUS9502576
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPCPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US95-02576-23

Query Match 100.0%; Score 1733; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPQCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQFANSQNSQSLSELYVFWQDQ 60
DB 1 MDPQCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQFANSQNSQSLSELYVFWQDQ 60
QY 61 ENLYAVNEVYLGKREKFDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYQCIIHKKKPTGM 120
DB 61 ENLYAVNEVYLGKREKFDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYQCIIHKKKPTGM 120
QY 121 IRIHQMSSELYLANFQPEIIVPISNTENYINLTCSIHGYPEPKKMSVLLRTKNSI 180
DB 121 IRIHQMSSELYLANFQPEIIVPISNTENYINLTCSIHGYPEPKKMSVLLRTKNSI 180
QY 181 EYDGIQMSQDNVTELYDVSTISLSVSPDYTSNMRTFCLILETDKTRLLSPFSIELEDQ 240
DB 181 EYDGIQMSQDNVTELYDVSTISLSVSPDYTSNMRTFCLILETDKTRLLSPFSIELEDQ 240
QY 241 PPPDHIMTITAVLPTVIICVAVFCLILMKKKRRPRNSYKCGTNTMERESQTKKREK 300
DB 241 PPPDHIMTITAVLPTVIICVAVFCLILMKKKRRPRNSYKCGTNTMERESQTKKREK 300
QY 301 IHIPERSDEAQRVFKSSKTSKCDKSDTCF 329
DB 301 IHIPERSDEAQRVFKSSKTSKCDKSDTCF 329

RESULT 5
PCT-US94-09642-2
Sequence 2, Application PC/TUS9409642
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation, M-3-W
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940-1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh IICx
OPERATING SYSTEM: System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09642
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,606
FILING DATE: 13-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,882
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0390K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-09642-2

Query Match 97.9%; Score 1696; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 6,8e-151;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGSLNITLFFVNAFLILSGAAPLIKQAYFNETADLPQCFANSONOSLSLAVFWMDQENLVIN 66
Db 1 MGSLNITLFFVNAFLILSGAAPLIKQAYFNETADLPQCFANSONOSLSLAVFWMDQENLVIN 60
QY 67 EYLIGKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHHKKPTGMIRIHOM 126
Db 61 EYLIGKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHHKKPTGMIRIHOM 120
QY 127 NSELVLANFSQPEIPIVINSITENVYINTLCSSIHGYPEPKKMSVLLRTKNSITIEDGIM 186
Db 121 NSELVLANFSQPEIPIVINSITENVYINTLCSSIHGYPEPKKMSVLLRTKNSITIEDGIM 180
QY 187 OKSDONTVELDYVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQPPDHI 246
Db 181 OKSDONTVELDYVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQPPDHI 240
QY 247 PWITAVLPYIICVWVFCILIMKKKKRRNSYKCGTNTMERESBQTKREKHIPER 306
Db 241 PWITAVLPYIICVWVFCILIMKKKKRRNSYKCGTNTMERESBQTKREKHIPER 300
QY 307 SDEAORVFKSKTSSCDKSDTCF 329
Db 301 SDEAORVFKSKTSSCDKSDTCF 323

RESULT 6
US-08-456-104-4
Sequence/4, Application US/08456104
Patent No. 5861310

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-4

Query Match 42.9%; Score 743.5; DB 2; Length 309;
Best Local Similarity 51.5%; Pred. No. 8,1e-62;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPCCTMGSLNITLFFVNAFLILSGAAPLIKQAYFNETADLPQCFANSONOSLSLAVFWMDQ 60
Db 1 MDPCCTMGSLNITLFFVNAFLILSGAAPLIKQAYFNETADLPQCFANSONOSLSLAVFWMDQ 60
QY 61 ENLVANFVYIGKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHHKKPTGM 120
Db 61 ENLVANFVYIGKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHHKKPTGM 120
QY 121 IRIHOMNSELVLANFSQPEIPIVINSITENVYINTLCSSIHGYPEPKKMSVLLRTKNSIT 180
Db 121 IRIHOMNSELVLANFSQPEIPIVINSITENVYINTLCSSIHGYPEPKKMSVLLRTKNSIT 180
QY 181 EYDGINOKSDONTVELDYVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQ 240
Db 179 EYDGINOKSDONTVELDYVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQ 238
QY 241 PPPDHIPW--ITAVLPVYIICVWVFCILIMKKKKRRNSYKCGTNTMERESBQTKR 298
Db 239 PPPDHIPW--ITAVLPVYIICVWVFCILIMKKKKRRNSYKCGTNTMERESBQTKR 289
QY 299 EKHIPPE 305
Db 290 EKHIPPE 296

RESULT 7

US-08-479-744A-23
Sequence 23, Application US/08479744A
Patent No. 6084067

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773


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? REFERENCE/DOCKET NUMBER: BWT-120CPDC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)227-5941
? INFORMATION FOR SEO ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 314 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? PCT-US95-02576-13

```

REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-744A-47

Query Match 29.8%; Score 517; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 ANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLLRTKNSTIEYDGIIMKSDNY 193
1 ANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLLRTKNSTIEYDGIIMKSDNY 60

QY 194 TELYDVISISVSFPDVTSMNTIFCLLETDKTRLLSPFSIE 235
61 TELYDVISISVSFPDVTSMNTIFCLLETDKTRLLSPFSIE 102

RESULT 12
PCT-US95-02576-32

Sequence 32, Application PC/TUS9502576
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules

TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510
CITY: Boston

STATE: Massachusetts
COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02576
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697

FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:

NAME: Mandiagouras, Amy E.
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BMT-120CPPC
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US95-02576-32

Query Match 18.9%; Score 328; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.4e-24;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 KWKKKRPRNSYKCGTNTMERESQTKRKREKIHIPERSDEARVFKSSKTSCKSDKSDTC 328

|||||
Db 1 KWKKKRPRNSYKCGTNTMERESQTKRKREKIHIPERSDEARVFKSSKTSCKSDKSDTC 60
QY 329 F 329
Db 61 F 61

RESULT 13

PCT-US95-02576-2
Sequence 2, Application PC/TUS9502576

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules

TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510
CITY: Boston

STATE: Massachusetts
COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02576
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697

FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:

NAME: Mandiagouras, Amy E.
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BMT-120CPPC
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 320 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US95-02576-2

Query Match 14.2%; Score 245.5; DB 4; Length 320;
Best Local Similarity 30.4%; Pred. No. 3.3e-15;
Matches 82; Conservative 51; Mismatches 100; Indels 37; Gaps 14;

QY 11 NILEVNAFLISGAAPKIAFYNETAD--LPCQFANSQNSLSLVFWQOENLYLNE 67
11 NILEVNAFLISGAAPKIAFYNETAD--LPCQFANSQNSLSLVFWQOENLYLNE 67

Db 22 NILEVNLIRLSQVSDVDQLSKSVKDKVLLPCRY-NSPHEDESEIRIYWKHNDVILS- 79
22 NILEVNLIRLSQVSDVDQLSKSVKDKVLLPCRY-NSPHEDESEIRIYWKHNDVILS- 79

QY 68 VYLGKEKFPDSVHAKYMGKRSFSDSWTLRLHNLQIKDKLYGICIIHHKKPTGMIRI-HQM 126
68 VYLGKEKFPDSVHAKYMGKRSFSDSWTLRLHNLQIKDKLYGICIIHHKKPTGMIRI-HQM 126

Db 80 VYAGKLR--VWPEYKRNRLYDNTYTLILGLVLSDRGYSCVY-QKKEGTYEYKHLA 135
80 VYAGKLR--VWPEYKRNRLYDNTYTLILGLVLSDRGYSCVY-QKKEGTYEYKHLA 135

QY 127 NSELVLANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLLRTKNSTIE 181
127 NSELVLANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLLRTKNSTIE 181

Db 136 LVKLSIKADSTNTNITESGKPSADTK-RITCFASGGFPKP-RFSLVLENGRELPGIWTI- 192
136 LVKLSIKADSTNTNITESGKPSADTK-RITCFASGGFPKP-RFSLVLENGRELPGIWTI- 192

QY 182 YDGIIMKSDNYTELVDVSISSVSFPDVTSMNTIFCLLETDKTRLLSPFSIELEDPQ 241
182 YDGIIMKSDNYTELVDVSISSVSFPDVTSMNTIFCLLETDKTRLLSPFSIELEDPQ 241

Db 193 -----SQPSESLYTISSQIDF---NTNRNTIKCLIKYGDAR-VSDFTWE-KRPED 240
193 -----SQPSESLYTISSQIDF---NTNRNTIKCLIKYGDAR-VSDFTWE-KRPED 240

QY 242 PPDHLPWIT-----AVLPYLIICVWVFC 264
242 PPDHLPWIT-----AVLPYLIICVWVFC 264

Db 241 PPDSKNTLVLFAGAGCAVITVVIYIIRK 270
241 PPDSKNTLVLFAGAGCAVITVVIYIIRK 270

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W09503408-A.
02-FEB-1995.
26-JUL-1994; 94WO-US08423.
26-JUL-1993; 93US-0101624.
19-AUG-1993; 93US-0109333.
03-NOV-1993; 93US-0147773.
(DAND) DANA FARBER CANCER INST INC.
(REPK) REPLIGEN CORP.
Freeman GJ, Gray GS, Greenfield E, Nadler LM,
WPI: 1995-075236/10.
N-PSDB; Q81351.
Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
for enhancing or suppressing T-cell mediated immune responses
Claim 35; Fig 8; 175pp; English.

CC A cDNA library was constructed in the pCDM8 vector using poly A+ RNA
CC from the human anti-19M activated B cells. Four clones were strongly
CC positive for Br-2 expression by indirect immunofluorescence using
CC CytA41g and flow cytometric analysis. The Br-2 cDNA insert in clone
CC 29 was sequenced in the pCDM8 expression vector employing the
CC following strategy. Initial sequencing was performed using
CC sequencing primers T7 (081352), CDM8R (081353) (Invitrogen)
CC to pCDM8 vector sequences adjacent to the clone Br-2 cDNA. Sequencing
CC was performed using dye terminator chemistry and an ABI automated DNA
CC sequencer. DNA sequence obtained using these primers was used to design
CC additional sequencing primers (see 081354-081363). This cycle of
CC sequencing and selection of additional primers was continued until
CC the Br-2 cDNA was completely sequenced on both strands. The human
CC Br-2 clone 29 cDNA sequence is given in 081351. The predicted
CC protein sequence (R67984) exhibits many features common to other
CC type 1 Ig superfamily membrane proteins. Following cleavage of the
CC signal peptide the resulting membrane-bound protein would have an
CC unmodified mol. wt. of approx. 34 kDa. The extracellular domain
CC contains eight potential N-linked glycosylation sites. E. coli
CC transfected with a vector containing the cDNA insert of clone 29 was
CC deposited under ATCC 69357 on July 26 1993.

Query Match	100.0%	Score 1733;	DB 16;	Length 329;
Best Local Similarity	100.0%	Pred. No. 4.2e-151;		
Matches 329; Conservative	0;	Mismatches	0;	Indels 0;
QY	1	MDPQCTWGLSNTLFPMAFLISGAPLAKIOAYENFNADLPCCRFANSQNSLSLWYFWQDQ	60	
Db	1	mopqctunglsmllfymatflsgaaaplksqayfneadlpcgfamsqngslslwvfwqdg	60	
QY	61	ENLVNENYLYKEKEKEDSVSHSKYMGRTSPDSQSWTLRLNLQIKDGLVOCIRHHKKPTGM	120	
Db	61	enlvnenylykexkedsvshskymgrtstfstdsdwtlrlmlqtkdglvqcllhhkkptgm	120	
QY	121	IRIHOMNSELVLNFSQPEIIVPISNITENYVNLTCSSIHGYPKKMSVLLRRKNSTI	180	
Db	121	irihomselvlnanfsqpeivpislntlenyvnltcslsngypkkmsvllrrknsti	180	
QY	181	EYDSIMQKSQDNVELDVYSISLSVSPDVDVSNMTIFCILETDKTRLSSPFSIELEDQD	240	
Db	181	eydldmqksqgnvelxvdsislsvsfdvtsnmtifclletdktrllspsfslsedpq	240	
QY	241	PPPHIMITAVLVTIIVICVAVFCILILMKKKKKRPRRSYKCGNTTMRRESEQYTKREK	300	
Db	241	ppphimvltavlpvtlvcvmvfclllwkwkkktrpmsycgnttmereseqgklkrek	300	

XX M09640915-A2.
FN 19-DEC-1996.
PD 06-JUN-1996; 96WO-US09052.
XX 07-JUN-1995; 95US-0479744.
PR (DAND) DANA FARBER CANCER INST INC.
PA (REPK) REPLIGEN CORP.
XX Freeman GJ, Gray GS, Nadler LM;
PI WPI: 1997-077269/07.
XX DR N-PSDB; 749181.
XX DNA encoding a B7-2 fusion protein - used to enhance or down
PT regulate B lymphocyte antigens
XX
XX Claim 4; Page 95-96; 171pp; English.
PS
XX Human B-lymphocyte antigen B7-2 (W08467) is a CTLA4/CD28 ligand
CC which costimulates T cell activation. It shows 26% amino acid
CC identity to human B7-1. Its sequence was deduced from a cDNA
CC clone (T49181) isolated from an anti-IGM activated B cell cDNA
CC library. Novel fusion proteins comprising the extracellular domain,
CC variable region-like or constant region-like domains of B7-2 (see
CC also W08472-73) and e.g. an immunoglobulin heavy chain constant
CC region can be expressed in host cells and used to enhance or
CC suppress T cell-mediated immune responses.
CC
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 18; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.2e-151;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDPQCTMGLSNIILFVMAFLLSGAPLKIQAIFNETADLPQCFANSONOSLSELVFWMODQ 60
DB 1 mdpqctmglsnllfvmatlfsqaaplkiqayfnetadlpcqfansqngsiseilvfwqdq 60
OY 61 ENLVANEVYLGEKEKFDVSHSKYMGRTSFDSDSWTLRLNLQIKDKGLYOCIIHKKKPTGM 120
DB 61 enlvanevylgkexfdsvshskymgrtsfddswtlrlnlqikdkglyociihkkkptgm 120
OY 121 IRIHQNSELSYLANFSQPEIPIISNTITENVYINLTCSHIGYPERKMSVLLRTKNSTI 180
DB 121 irihqnmseisylanfsqpeipisntitenyynltcsshigyperkmsvllrtknsti 180
OY 181 EYDGIQKSDQNTVELYVDSISLSVSPDVTSNMNITFCILETQTRLLSPFSIELEDPO 240
DB 181 eydgiqksgdnvteilydvsislsvsfpdvtsnmnifciletdktrllspfsieleddp 240
OY 241 PPPDHIPMTAVLPTVITICVWVECLILMKWKKKRPNSYKCGTNTMERESQTKKREK 300
DB 241 pppdhlpmtavlpvtvicvwvfcililwkwwkkrrpnsykcgtnumereesqtkkrek 300
OY 301 IHIPEBSDEAQRVFKSKTSCKSDKSDTCF 329
DB 301 ihipersdeaqrvfkssktscksdctcf 329

RESULT 3
ID W73638 standard; Protein; 329 AA.
XX
AC W73638;
XX
DT 23-MAR-1999 (first entry)
XX
DE Human B7-2 antigen.

XX B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
KM CTLA4 ligand; therapy; T-cell response; human.
XX Homo sapiens.
OS US5861310-A.
XX 19-JAN-1999.
PD 30-MAY-1995; 95US-0456104.
XX 30-MAY-1995; 95US-0456104.
PR 03-NOV-1993; 93US-0147773.
XX
XX (DAND) DANA FARBER CANCER INST INC.
XX Freeman GJ, Gray GS, Nadler LM;
XX WPI: 1999-130394/11.
XX DR N-PSDB; V55784.
XX Tumour cell transfected to express B7-2 molecule - useful for tumour
PT therapy by stimulating T-cell response
XX
XX Claim 10; Column 27-30; 27pp; English.
PS
XX This sequence is the human B7-2 antigen, which can be used in the
CC method of the invention. The method is for transfecting an isolated
CC mammalian tumour cell with an exogenous nucleic acid molecule encoding a
CC mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
CC tumour cell is capable of costimulating a T cell and is capable of
CC binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
CC by stimulating a T-cell response against tumour cells in vivo.
CC
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 20; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.2e-151;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDPQCTMGLSNIILFVMAFLLSGAPLKIQAIFNETADLPQCFANSONOSLSELVFWMODQ 60
DB 1 mdpqctmglsnllfvmatlfsqaaplkiqayfnetadlpcqfansqngsiseilvfwqdq 60
OY 61 ENLVANEVYLGEKEKFDVSHSKYMGRTSFDSDSWTLRLNLQIKDKGLYOCIIHKKKPTGM 120
DB 61 enlvanevylgkexfdsvshskymgrtsfddswtlrlnlqikdkglyociihkkkptgm 120
OY 121 IRIHQNSELSYLANFSQPEIPIISNTITENVYINLTCSHIGYPERKMSVLLRTKNSTI 180
DB 121 irihqnmseisylanfsqpeipisntitenyynltcsshigyperkmsvllrtknsti 180
OY 181 EYDGIQKSDQNTVELYVDSISLSVSPDVTSNMNITFCILETQTRLLSPFSIELEDPO 240
DB 181 eydgiqksgdnvteilydvsislsvsfpdvtsnmnifciletdktrllspfsieleddp 240
OY 241 PPPDHIPMTAVLPTVITICVWVECLILMKWKKKRPNSYKCGTNTMERESQTKKREK 300
DB 241 pppdhlpmtavlpvtvicvwvfcililwkwwkkrrpnsykcgtnumereesqtkkrek 300
OY 301 IHIPEBSDEAQRVFKSKTSCKSDKSDTCF 329
DB 301 ihipersdeaqrvfkssktscksdctcf 329

RESULT 4
ID R71478 standard; Protein; 323 AA.
XX
AC R71478;
XX

```
DT 09-OCT-1995 (first entry)
XX
DE B70 type B antigen which binds CTLA-4 and CD28.
XX
KM B70 antigen; CTLA-4; CD28; T cell response.
XX
OS Homo sapiens.
XX
PN W09506738-A.
XX
PD 09-MAR-1995.
XX
PF 02-SEP-1994; 94MO-US09642.
XX
PR 03-SEP-1993; 93US-0116882.
PR 13-SEP-1993; 93US-0120606.
XX
PA (AZUM/) AZUMA M.
PA (OKUM/) OKUMURA K.
PA (SCHE ) SCHERING CORP.
XX
PI Azuma M, Lanier LL, Okumura K, Phillips JH;
PI Somoza Diaz-Sarmiento M;
DR WPI: 1995-115453/15.
DR N-PSDB; Q85873.
XX
PT New CTLA-4/CD28 binding protein, B70 - used to develop prods for
PT modulating the physiology, growth or development of cells.
XX
PS Claim 3; Page 44-45; 55pp; English.
XX
CC B70 is a natural proteinaceous binding partner for CTLA-4 and CD28
CC markers/antigens. It is distinct from the known B7/BBI marker. It is
CC representative of type B markers/antigens/binding partners. The
CC type A markers/binding partners include both CTLA-4 and CD28 and
CC antibodies specific for B70, and are characterised, in part, by the
CC property of serving as a binding partner for B70. A cDNA encoding a
CC B70 antigen was cloned by expression cloning using mAb IT2.236 to
CC select COS7 cells transfected with a cDNA library cloned into the
CC pEF4 vector. The library was made from RNA isolated from a human
CC EBV-transformed B-lymphoblastoid cell line JY.
XX
SQ Sequence 323 AA;
Query Match 97.9%; Score 1696; DB 16; Length 323;
Best Local Similarity 100.0%; Pred. No. 1e-147;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGSLNILEVNAFLLSGAAPLKIQAYFNETADLPQCFANSONOSLSELVFWMOQENLVN 66
DB 1 mgsnllfmaflfllsgaaplkiaqayfnetadlpqcfansqngslselvfwqdenlvn 60
QY 67 EYVLGKEKFDVSHSKYWGRTSPDSWTLRLHNLQIKDKGLYOCIIHKKPTGMRIRHQM 126
DB 61 evylgkekfdsvshskymgrtsfidsdswtlrlhnlqldkglgycilhhkptgmirlhgm 120
QY 127 NSELVLANSPQPEIVISNITENVYINLTCSSIHGYPEPKKMSVLLRTNSTIENDGIM 186
DB 121 nselvliansqpeivpislntenvylnltcssihgypepkmsvllrtknstleyqim 180
QY 187 OKSDQWNTLEYDVYSISVSFPPVTSNMTFCILETPDKTLLSSPSEILEDQPPDH 246
DB 181 qksqdnvteleydvysisvsfpvtsnmtfciletpdktrllsspsieledqppdh 240
QY 247 PWTAVLPVILICVMVFCILIMWKKRRPRNSYKCGTNTMERESQTKRKREKIHIPER 306
DB 244 pwtavlpvlicvmvfclilwkkrrprnsykcgtntmeresqtkrkrekibhper 300
QY 307 SDEAQRVFKSSKSSGDKSPTCF 329
DB 301 sdeaqrvfkssksscdkscdtcf 323
```

```
RESULT 5
ID Y44290
XX Y44290 standard; Protein; 323 AA.
XX
AC Y44290;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human B7.2 co-stimulatory molecule.
XX
KW Human B7.2 co-stimulatory molecule; antigen presenting cell;
KW immune response; cell surface receptor; Major histocompatibility complex;
KW MHC classII; proton motor force; mitochondrial membrane potential;
KW mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN W09953953-A2.
XX
PD 28-OCT-1999.
XX
PF 30-MAR-1999; 99MO-US06874.
XX
PR 17-APR-1998; 98US-0082250.
PR 29-JUL-1998; 98US-0094519.
PR 24-SEP-1998; 98US-0101580.
XX
PA (UYVE-) UNIV VERMONT.
XX
PI Newell MK;
XX
DR WPI: 2000-096773/08.
DR N-PSDB; Z29321.
XX
PT Use of cell surface and membrane characteristics for developing
PT products for treating cancers, autoimmune diseases or neurodegenerative
XX
PS Disclosure; Page 116-117; 123pp; English.
XX
CC The present sequence is human B7.2 co-stimulatory molecule. This is
CC a glycoprotein on the surface of antigen presenting cells. This is
CC involved in stimulation of an immune response by its ability to interact
CC with various immune cell surface receptors. The regulation of cell
CC surface expression of MHC classII and co-stimulatory molecule B7 can be
CC manipulated by regulating the intracellular dissipation of proton motor
CC force which can be assessed in terms of mitochondrial membrane potential.
CC These methods can be used for regulating cell growth and division to
CC control disease processes by manipulating mitochondrial metabolism and
CC the expression of cell surface immune proteins. They can be used for
CC treating diseases associated with excessive cellular division, aberrant
CC differentiation, and premature cellular death, e.g. cancers, autoimmune
CC diseases, neurodegenerative disorders etc.
XX
SQ Sequence 323 AA;
Query Match 97.9%; Score 1696; DB 21; Length 323;
Best Local Similarity 100.0%; Pred. No. 1e-147;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGSLNILEVNAFLLSGAAPLKIQAYFNETADLPQCFANSONOSLSELVFWMOQENLVN 66
DB 1 mgsnllfmaflfllsgaaplkiaqayfnetadlpqcfansqngslselvfwqdenlvn 60
QY 67 EYVLGKEKFDVSHSKYWGRTSPDSWTLRLHNLQIKDKGLYOCIIHKKPTGMRIRHQM 126
DB 61 evylgkekfdsvshskymgrtsfidsdswtlrlhnlqldkglgycilhhkptgmirlhgm 120
QY 127 NSELVLANSPQPEIVISNITENVYINLTCSSIHGYPEPKKMSVLLRTNSTIENDGIM 186
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Db 121 nselavlafspglvplnsientenyintlcassibgypepkkmvslrltrknsitiedygm 180
QY 187 QKSQNMVELYVSVISLSVSPDYVSNMTIFCLLETDKTRLISPPSTIELEDPQPPDHI 246
Db 181 qksqdvneilydvsislsvstfsvtsnmtlfciletdktrllsspfisleddpqpdpdhi 240
QY 247 PWITAVLPVLIICVAVFCLLMKMKKKRPRNSYKGTWMTMERSEQTKRKREKTHIPER 306
Db 241 pwitavlpvliicvavfclllmkmkkkripnsykcgtunmeresegtkrkrehliper 300
QY 307 SDEAQRVFKSSKRTSSCDKSDTICF 329
Db 301 sdeaqrvfksskrtsscdskdctcf 323

RESULT 6
W42339
ID W42339 standard; Protein; 260 AA.
AC W42339;
XX
DT 22-JUN-1998 (first entry)
DE CD86 extracellular domain.
XX
KW Hexameric fusion protein; IgA; alpha-tp; tailpiece; antibody;
KW CD86; CD28; CTLA-4; vaccine; diagnosis; binding assay; screening;
KW human; ds.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide 1..25
FT /label= Sig_peptide
FT Protein 26..260
FT /label= Mat_protein
FT Peptide 245..250
FT /label= Ig_hinge
XX
PN W09747732-A2.
XX
PD 18-DEC-1997.
XX
PE 13-JUN-1997; 97WO-US12599.
XX
PR 21-FEB-1997; 97US-0038915.
PR 14-JUN-1996; 96US-001934.
PR 19-FEB-1997; 97US-0043948.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Chaikin MA, Lyn SDP, Sweet RW, Truneh A;
XX
DR WPI; 1998-052299/05.
DR N-PSDB; V03230.
XX
PT Hexameric fusion protein containing IgA antibody fragment - used for
PT stimulating CD28 positive cells, or suppressing CTLA-4 positive
PT cells
XX
PS Example 1; Fig 5A-B; 105pp; English.
XX
CC This protein comprises the signal region and extracellular
CC domain of human CD86 encoded by a portion (see V03230) of
CC plasmid CD86fcalphaplknk. This plasmid encodes a fusion protein
CC comprising the CD86 signal peptide and extracellular domain
CC grafted to a human IgG1 heavy chain Fc region and the tailpiece
CC region (alpha-tp) (see W42344) of human IgA heavy chain. The
CC processed fusion protein has been expressed as a hexamer in COS
CC cells. The invention relates to novel hexameric fusion proteins
CC comprising a dimeric binding protein such as CD86 provided at its
CC C-terminus with a tailpiece that has the activity of alpha-tp. The

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CC tailpiece provides the fusion protein with the ability to form
CC stable hexamers. Also claimed are polynucleotides encoding the
CC hexameric fusion proteins, vectors, recombinant host cells and a
CC method for producing the hexamers. The fusion protein is useful in
CC therapeutics and vaccines, and is particularly well suited for
CC applications for which the binding protein from which it is derived
CC is unsatisfactory because of low binding affinity or for
CC applications where multivalency is desired. Applications include
CC diagnostics, binding assays and screening assays. CD86-Ig-alpha-tp
CC fusion protein is used in claimed methods for stimulating CD28
CC positive cells or suppressing CTLA-4 positive cells.
XX
SQ Sequence 260 AA:

Query Match 74.0%; Score 1282; DB 19; length 260;
Best Local Similarity 99.6%; Pred. No. 7.3e-110;
Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPOCTMGISNLIFFVMAFLISGAAPLKIAVFRFETADLFCQFRANSQNSISELYVWQDQ 60
Db 1 mdpoctmgisnllfymaflisgaaplkiaayfrfetraddlpcqfransqnsiselyvtwqdg 60
QY 61 ENLVINEVYLGKEKFPDSVHSKTYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHHKKPTGM 120
Db 61 enlvinevylgkekfsdsvhsksymgrtfsdswtlrlhnlqldkgllyocilhhkxptgm 120
QY 121 IRIHONSLSVLANFSOPEIPIVSNITENYINLTCSSIHGYPEPKKMSVLLRTKNSIT 180
Db 121 irihqunselsvlanfsgeipvisnitenyintlcassibgypepkkmvslrltrknsit 180
QY 181 EYDGIWQKSDQWVELYDVSVISLSVSPDYVSNMTIFCLLETDKTRLISPPSTIELEDPQ 240
Db 181 eydgiwqksqdwtelydvsislsvstfsvtsnmtlfciletdktrllsspfisleddp 240
QY 241 PPPDHP 247
Db 241 pppdhpep 247

RESULT 7
W86005
ID W86005 standard; Protein; 246 AA.
XX
AC W86005;
XX
DT 15-MAR-1999 (first entry)
DE Human B7-2 extracellular domain and linker.
XX
KW Tumour interacting protein; cancer; gene therapy; vector;
KW 5T4 antigen; monoclonal antibody; single chain antibody;
KW mouse; human; B7-2; co-stimulatory molecule.
XX
OS Chimeric - Homo sapiens.
XX
FH Chimeric - synthetic.
XX
FH Key
FH Peptide 1..16
FT /label= Sig_peptide
FT Protein 17..241
FT /label= Mat_protein
FT /note= "B7-2 extracellular domain"
FT Peptide 242..246
FT /label= Linker
XX
PN W09855607-A2.
XX
PD 10-DEC-1998.
XX
PR 04-JUN-1998; 98WO-GB01627.
XX
PR 04-JUL-1997; 97GB-0014230.

```

PR 04-JUN-1997: 97GB-0011579.
PR 20-JUN-1997: 97GB-0013150.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Babbington CR, Carroll MW, Ellard FM, Kingsman SM;
PI Myers KA;
XX
XX WPI: 1999-059910/05.
DR N-PSDB: V80293.
XX
XX New vector encoding a tumour interacting protein for treating cancer
PT - contains a desired nucleotide sequence and/or protein which
PT recognises tumours, and is used as a gene delivery system to treat
PT cancer
XX
XX Example 5; Fig 4; 82pp; English.
PS
XX This polypeptide comprises the extracellular domain (amino acids
CC 1-215) of human co-stimulatory molecule B7-2 joined to a C-terminal
CC flexible peptide linker. It is part of B7-2.5T4.1 co-stimulatory
CC domain, a fusion protein comprising the B7-2 extracellular domain
CC joined via the linker to an scFv (see W86002) derived from murine
CC 5T4 monoclonal antibody. B7-2.5T4.1 cDNA (see V80293) can be
CC inserted into vector pCI to allow expression of the fusion protein
CC in mammalian cells. The trophoblast cell surface antigen defined
CC by 5T4 is expressed at high levels on the cells of a wide variety
CC of human tumours. The invention relates to a vector comprising a
CC nucleotide sequence coding for a tumour interacting protein (TIP)
CC and optionally a nucleotide sequence of interest (NOI) which
CC encodes a protein of interest (POI), the vector being capable of
CC delivering the NOI and/or POI to the tumour recognised by the TIP.
CC Delivery can be in vivo or ex vivo. The vector is used to treat
CC cancer, and may also be used as a gene delivery system for
CC introducing at least 1 gene encoding a TIP (preferably a tumour
CC binding protein) into a haematopoietic cell lineage. B7-2 is
CC expected to bind specifically to CD28 and CTLA-4 present on human
CC T-cells.
XX
SQ Sequence 246 AA:

Query Match 72.2%; Score 1252; DB 20; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.8e-107;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQOFANSQNSQSELVVEWQDENLVN 66
Db 1 mglsnllfvmalfllsgaaplkigayfnetadlpqofansqnselslvfwqdenlvln 60
QY 67 EYVIGKEKFDVSHSKYMRSTFSDSDSWTLRLHNIQIRKXGIXOCIIHKKRTGMRHQM 126
Db 61 evyigkekfdsvhskymgrtsfidsdswclrlhniqirkxgilyqclihhkkpctgmrlrhqm 120
QY 127 NSELVLANFSQPEIVPISNTENYINLTCSSIHGYPEPKMSVLRTKSTTEYDQIM 186
Db 121 nselvlianfsqpeivpnsntenyinlntcssihgypepkmsvllrtkstteydgim 180
QY 187 OKSODNTELYDVSISLSVSPDYTSNMRTFCILETDKTRLLSPFSTLEDDPPDPDH 246
Db 181 qksodntelydvsislsvsfpdytsnmrtfciletdktrllspfstsleddppdpdhi 240
QY 247 P 247
Db 241 P 241

RESULT 8
ID W90209 standard; Protein; 244 AA.
XX
AC W90209;
XX

DT 10-MAY-1999 (first entry)
XX
XX hb7.This soluble fusion protein.
DE
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KW CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy; human; hb7.1hs.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..23 /note= "potential eukaryotic secretory signal
FT /note= "peptide"
FT Domain 24..238
FT /note= "human B7.2 (mature protein) extracellular
FT Peptide 239..244 /note= "histidine detection/purification tag"
FT
FT
XX W09858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998: 98WO-EP03791.
XX
XX 20-JUN-1997: 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX WPI: 1999-105615/09.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection
PT
XX
XX Example 3.1.3; Fig 5; 182pp; English.
PS
XX This 28 kDa soluble fusion protein, termed hb7.2hs, is composed
CC of human co-stimulatory molecule B7.2 extracellular domain fused
CC C-terminally to a hexahistidine detection/purification tag. It
CC was produced by PCR amplification (see X01603-04) of hb7.2 cDNA
CC in pCDNAhB7.2 (ICCG2307), insertion of the PCR fragment into
CC baculoviral transfer vector PACS62 and expression in Sf9 Spodoptera
CC frugiperda insect cells. The invention relates to molecules such
CC as antibodies, trivalent and tetravalent antibodies and small
CC antigen binding peptides which can cross-link, or cross-react
CC with, B7.1 and B7.2 expressed on professional antigen presenting
CC cells leading to the inhibition of antigen-specific T cell
CC activation. Methods to produce such molecules are provided. The
CC molecules are used to treat or prevent diseases of the immune
CC system, in particular graft rejection, graft versus host disease,
CC allergy and autoimmune diseases (claimed).
XX
SQ Sequence 244 AA:

Query Match 71.6%; Score 1241; DB 20; Length 244;
Best Local Similarity 100.0%; Pred. No. 3.9e-106;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQOFANSQNSQSELVVEWQDENLVN 66
Db 1 mglsnllfvmalfllsgaaplkigayfnetadlpqofansqnselslvfwqdenlvln 60
QY 67 EYVIGKEKFDVSHSKYMRSTFSDSDSWTLRLHNIQIRKXGIXOCIIHKKRTGMRHQM 126
Db 61 evyigkekfdsvhskymgrtsfidsdswclrlhniqirkxgilyqclihhkkpctgmrlrhqm 120
QY 127 NSELVLANFSQPEIVPISNTENYINLTCSSIHGYPEPKMSVLRTKSTTEYDQIM 186

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Db 121 nselsvlanfsgpeivpsnltentvynlntcssihgypepkmsvllrtknsitleydgim 180
OY 187 OKSDQNTVELYDVSISSVSFPDVTSMNTIFCILETDKTRLISSPFSIELEDPPPPDH 245
    |||||||
Db 181 qksqdnvteiydvsislsvsfpdvtsmntlfciletdktrlisspsfieleddppppdh 239

RESULT 9
W90207
ID W90207 standard: Protein; 477 AA.
AC W90207;
XX
XX
DT 10-MAY-1999 (first entry)
DE hb7.2Fc soluble fusion protein.
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KM CD86; T cell activation; inhibitor; graft versus host disease;
KM transplant rejection; allograft rejection; autoimmune disease;
KM allergy; therapy; human; antibody; hb7.1Fc.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT /note= "potential eukaryotic secretory signal"
FT /note= "peptide"
FT Domain 17..239
FT /note= "human B7.2 (mature protein) extracellular
FT Peptide 240..245
FT /note= "introduced by PCR cloning strategy"
FT Protein 246..477
FT /note= "human IgG1-Fc (hinge-CH2-CH3)"
XX
XX W09858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Bosman A, Buyse M, Lorre K, Sablon E;
PI WPI, 1999-105615/09.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection
XX
XX Example 3.1.1.3; Fig 3; 183pp; English.
XX
XX This 54 kDa soluble fusion protein, termed hb7.2Fc, is composed of
CC human co-stimulatory molecule B7.2 extracellular domain fused
CC C-terminally to human IgG1-Fc. It was produced by PCR
CC amplification of hb7.2 cDNA in plasmid pCDNAneo-hb7.2, and
CC insertion of the amplified cDNA into pVc-Fc (ICCG3048), resulting
CC in pVc-hb7.2-Fc (ICCG3004) baculotransfer plasmid. The invention
CC relates to molecules such as diabodies, trivalent and tetravalent
CC antibodies and small antigen binding peptides which can cross-link,
CC or cross-react with, B7.1 and B7.2 expressed on professional
CC antigen presenting cells leading to the inhibition of
CC antigen-specific T cell activation. Methods to produce such
CC molecules are provided. The molecules are used to treat or prevent
CC diseases of the immune system, in particular graft rejection, graft
CC versus host disease, allergy and autoimmune diseases (claimed).
XX
XX Sequence 477 AA:
SQ

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```

Query Match 71.6%; Score 1241; DB 20; Length 477;
Best Local Similarity 100.0%; Pred. No. 1e-105;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 MGLSNILFVNAFFLLSGAAPKIOAFNETADLPQOFANSONOSLSELYVWQDQENLYIN 66
    |||||||
Db 1 mglsnllfmaflisgaaplkiaqyfnctadlpqofansqglselvrfwqdenlvln 60
OY 67 EYVLGKKEKFDPSVHSKYGRTSPDSWTLRLHNLQIKDKGLYOCIIHHKKPTGMIRIHQM 126
    |||||||
Db 61 evylgkkekfdsvhsakymgrtsfdswtlrlhnlqikdkglycclihhkkprtgmirihqm 120
OY 127 NSELVLANFSQPEIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSITIEYDGM 186
    |||||||
Db 121 nselsvlanfsgpeivpsnltentvynlntcssihgypepkmsvllrtknsitleydgim 180
OY 187 OKSDQNTVELYDVSISSVSFPDVTSMNTIFCILETDKTRLISSPFSIELEDPPPPDH 245
    |||||||
Db 181 qksqdnvteiydvsislsvsfpdvtsmntlfciletdktrlisspsfieleddppppdh 239

RESULT 10
Y41076
ID Y41076 standard: protein; 329 AA.
XX
XX Y41076;
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-2 protein.
DE
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX Canis familiaris.
XX
XX W09947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
PI WPI, 1999-571822/48.
XX
XX N-PSDB; 227913, 227915.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX Claim 4; Page 97-99; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
XX Sequence 329 AA:
SQ

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Query Match          57.9%; Score 1003; DB 20; Length 329;
Best Local Similarity 62.3%; Pred. No. 4,1e-84;
Matches 205; Conservative 47; Mismatches 71; Indels 6; Gaps 6;

QY 4 QCTMGLSNILFVMAFLISGAAPLKIQAYENETADLPCOFANSONOSLSELYVFMODQENL 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 rcthelmlilfvmclllygaasmksqayfntgelpchfnstqnlslidelvfwgqdkl 63

QY 64 VLVNVEYLKKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKKGLYOCIIHHKKPTGMRTI 123
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 64 vlyelyrgkempgvnhkkygrtfdkdmclrlhnlhngqikdgyqctvhhkpgkylvpm 123

QY 124 HOMNSELVIANFESQPEIPIPSNITENY-VYNLTGSSIHGYDEPKKMSVLTAKNSTREY 182
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 hgmmsdsvlanfsgpelmvsnrtensglnlccslygyipekemyflvktensstky 183

QY 183 DGIKOKSDNVTLEYDVSISSVSFPDVTSMNLTFCILETDKTRLLSPFSIELE-DEQP 241
   |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 dlymkksqmvntelynvslstsfvspe-asnvsilfcvliqlesmklpislynidahtkp 242

QY 242 PPDHPIPWITAVL-PTVITICVWVPCLLIMKKKKRRPNRSYKCGTNTMERESEOTKKREK 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 dgdhllwlaallvmlyllcgmwflfclrk-rkkkqpgpshectnkyerkeseqlker 301

QY 301 IHIPERSDEAQRVFKSSKTSKSCDSDTCF 329
   | ||||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db 302 yheterdeagcv-nlstkastgdnsttgf 329

RESULT 11
W14944 ID W14944 standard; Protein; 250 AA.
AC XX W14944;
XX XX

DT 16-JUN-1997 (first entry)
DE XX
XX XX Chimeric human/porcine CD86.
XX XX
XX XX Xenotransplantation; graft rejection; cell interaction; pig;
XX XX KM CD86; monoclonal antibody; chimeric antibody; diagnosis.
XX XX OS Chimeric Homo sapiens;
XX XX OS Chimeric Sus scrofa.
XX XX
XX XX Key Location/Qualifiers
XX XX FT Peptide 1..25
XX XX FT /label= Sig_peptide
XX XX FT Protein 26..250
XX XX FT /label= Mat_protein
XX XX FT Region 246..250
XX XX FT /label= Histidine_tag
XX XX
XX XX MO9711971-A1.
XX XX
XX XX 03-APR-1997.
XX XX
XX XX 27-SEP-1996; 96MO-US15575.
XX XX
XX XX 26-SEP-1996; 96US-0004489.
XX XX PR 26-SEP-1995; 95US-0004489.
XX XX
XX XX (ALEX-) ALEXION PHARM INC.
XX XX
XX XX Evans MJ, Mats LA, Mueller EF, Mueller JP, Rollins S;
XX XX PI Rother RP;
XX XX
XX XX WPI; 1997-212855/19.
XX XX DR N-PSDB; T62939.
XX XX
XX XX Antibodies binding to porcine but not human cell interaction
XX XX PT proteins - useful to treat and assay for rejection of xenografted
XX XX PT porcine organs, tissues or cells

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XX XX Disclosure; Page 69-70; 105pp; English.
PS PS
XX XX
CC CC A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has
CC CC amino acid residues 1-4 and 197-245 from human CD86, and amino
CC CC acids 5-196 from porcine CD86. It is encoded by a DNA construct
CC CC (T62939) obt'd. by PCR amplification of porcine sequences and
CC CC ligation to a sequence encoding the C-terminal region of human
CC CC CD86 19c domain. A signal sequence facilitates efficient
CC CC secretion from transfected mammalian cells. Antibodies to porcine
CC CC CD86 protein, P-selectin (see also W14945) and vascular cell
CC CC adhesion molecule (see also W14931-42) are useful for diagnosing
CC CC human rejection of porcine xenotransplants and for improving
CC CC xenotransplantation of porcine cells, tissues and organs into human
CC CC recipients.
SQ SQ Sequence 250 AA;

Query Match          57.2%; Score 991; DB 18; Length 250;
Best Local Similarity 78.0%; Pred. No. 3,3e-83;
Matches 191; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 1 MDPCTMGLSNILFVMAFLISGAAPLKIQAYENETADLPCOFANSONOSLSELYVFMODQ 60
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 mdpctmglnrlilvgwvlllsgaalskqayfnetgelpchfnstqnlslidelvfwgq 60

QY 61 ENLVNVEYLKKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKKGLYOCIIHHKKPTGM 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 dnlvlyelyrgkempgvnhkkygrtfdkdmclrlhnlhngqikdgyqctvhhkpgkyl 120

QY 121 IRIHOMNSELVIANFESQPEIPIPSNITENYVNLTCSSIHGYDEPKKMSVLTAKNSTI 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 vplnqmsdsvlanfsgpelmvsnrtensglnlccslygyipekemyflvktensst 180

QY 181 EYDGIKOKSDNVTLEYDVSISSVSFPDVTSMNLTFCILETDKTRLLSPFSIELEDPQ 240
   |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 ehdadmkksqmvntelynvslstsfvsfpdvtsnmflicletdktrllspsfiele 240

QY 241 PPPDH 245
   |||||
Db 241 pppdh 245

RESULT 12
Y41079 ID Y41079 standard; Protein; 332 AA.
XX XX
XX XX Y41079;
XX XX
XX XX 20-DEC-1999 (first entry)
XX XX
XX XX Feline B7-2 protein.
XX XX
XX XX B7; CT1A4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX XX KM allergic reaction; infectious disease; tumor development; feline;
XX XX KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX XX
XX XX Felis catus.
XX XX OS
XX XX OS
XX XX PN WO9947558-A2.
XX XX
XX XX 23-SEP-1999.
XX XX
XX XX 19-MAR-1999; 99MO-US06187.
XX XX PF
XX XX 19-MAR-1998; 98US-0078765.
XX XX PR 17-APR-1998; 98US-0062597.
XX XX
XX XX (HESK-) HESKA CORP.
XX XX PA
XX XX PI Sim G, Yang S, Sellins KS;
XX XX

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KW CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;
 KW FIV; feline leukemia virus; feline infectious peritonitis virus;
 KW feline panleukopenia virus; feline calicivirus; feline reovirus-3;
 KW feline rotavirus; feline coronavirus; feline syncytial virus;
 KW feline sarcoma virus; feline herpesvirus; feline Borna disease;
 KW rabies virus; Chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;
 KW parasite; autoimmune disease; transplant rejection; therapy.
 XX
 OS Felis domesticus.
 XX
 EN MO9957271-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99MO-US09502.
 XX
 PR 01-MAY-1998; 98US-0071699.
 XX
 PA (TEXA) TEXAS A & M SYSTEM.
 XX
 PI Collison EW, Hash SM, Choi I;
 DR WPI: 2000-052972/04.
 DR N-PSDB; 234785.
 XX
 PT Novel feline proteins used to produce feline vaccines which prevent
 PT infectious disease or to promote growth in homologous or heterologous
 PT species -
 XX
 PS Example 1A; Fig 3A; 186pp; English.
 XX
 CC The present sequence represents feline CD86 (B7-2) ligand, as
 CC predicted from isolated cDNA of peripheral blood mononuclear cells.
 CC The coexpression of CD86 with the costimulatory molecules CD28 (see
 CC Y32279) and a tumour antigen or an antigen from a pathogenic
 CC organism has the ability to activate or enhance activation of
 CC T-lymphocytes. Coexpression of CD86 with CTLA-4 (see Y32280) has
 CC the ability to regulate activation of T-lymphocytes. The invention
 CC provides isolated nucleic acids encoding feline CD86 ligand,
 CC feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
 CC (CD152) receptor, as well as vectors comprising the nucleic acids,
 CC and polypeptides encoded by the nucleic acids. It also provides
 CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
 CC further comprising immunogens derived from pathogens, especially
 CC feline immunodeficiency virus (FIV), feline leukemia virus,
 CC feline infectious peritonitis virus, feline panleukopenia virus,
 CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
 CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
 CC herpesvirus, feline Borna disease virus, rabies virus, Chlamydia,
 CC Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial
 CC pathogen, or parasite (all claimed). Vaccines capable of
 CC enhancing an immune response, and vaccines capable of suppressing
 CC an immune response (suitable for treating an autoimmune disease
 CC or tissue or organ transplant rejection) are claimed.
 CC
 XX
 SQ Sequence 329 AA;
 Query Match 52.1%; Score 903; DB 21; Length 329;
 Best Local Similarity 58.5%; Pred. No. 6.1e-75;
 Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;
 Oy 6 TMGSLNIFVNAFLISGAFLKIOAYFNEADLPQCFANSONOSLELYVFMODENL 65
 Db 7 tmgslhllvnaflisvsmksqayfinkgepchtfnsgnsldeylvfwgddqk 66
 Oy 66 NEVYLGEKEKEDSVHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIHHKPKPTGIRIQ 125
 Db 67 yelfrkgpnpvnlkkygtsfcdkdwltlrlnhvqkdkgyhcfihykygpkglvpmhg 126
 Oy 126 MNSLSTVLANSGPEIYPISTIPENV-YINLTGSSIHGVEPKKMSVLLRTKSTIEYNG 184
 Db 127 msdlsyvanlsgpeltvtsnrtengslndltcsslqgyepkemyfqintnsttkydt 186

Oy 185 IMKSDQNTWELDYDVSISLSPFDTSMNITFCILETDKTR-LLSPFSIELE--DPQP 241
 Db 187 vmksqgnvelynvsislpsfype-ahnvsvfcaikletlemllslpfnldaqpkd 245
 Oy 242 PPDHIIPIITVLEPT-VICVMVECLIMRKKRRPRNSYKCGTWTMESEQTKRREK 300
 Db 246 eqghflwlaavlvmtvfcgwafkflrk-rlkkkgpshcecllxkerkesqytrvp 304
 Oy 301 IHIPRSDENQRFKSKTSKTSCKS 325
 Db 305 yhvperdeaqcv-nllktasgdn 328
 RESULT 15
 Y41078
 ID Y41078 standard; protein; 280 AA.
 XX
 AC Y41078;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Canine B7-2s protein.
 XX
 KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; canine;
 KW graft rejection; inflammation; arthritis; atopic dermatitis.
 XX
 OS Canis familiaris.
 XX
 PN MO9947558-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99MO-US06187.
 XX
 PR 19-MAR-1998; 98US-0078765.
 PR 17-APR-1998; 98US-0062597.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Sellins KS;
 DR WPI: 1999-571822/48.
 DR N-PSDB; 227921, 227923.
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases
 XX
 PS Claim 4; Page 109-111; 148pp; English.
 XX
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 CC
 XX
 SQ Sequence 280 AA;
 Query Match 51.2%; Score 886.5; DB 20; Length 280;
 Best Local Similarity 55.7%; Pred. No. 1.6e-73;
 Matches 182; Conservative 40; Mismatches 54; Indels 51; Gaps 4;
 Oy 4 OCTGSLNIFVNAFLISGAFLKIOAYFNEADLPQCFANSONOSLELYVFMODENL 63
 Db 4 rctmelnllfwmlllygaasmksqayfinkgepchtfnsgnsldeylvfwgddqk 63
 Oy 64 VLNVEYLGEKEKEDSVHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIHHKPKPTGIRI 123

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Db      64  vlyelyrgkenpqnvhrykygrtsfdkdnwltlhnigdkgfygcfvnhkgpkglvpm 123
QY      124  HQMNSLSTLANFSQPEIYIPISNITEN-VYNLTGSSIHGYPEPKKMSVLLRTKNSTIEY 182
Db      124  hqmsdlsvlanfsqpeimvtsnrtensglntlcassigypepkemyflvktensstky 183
QY      183  DGIKMSODNVTETLVDVSTLSVSFPDYTSNMTIFCILETDKTRLLSSPFSIELEDPQPP 242
Db      184  dvmkxsgnvtelyvnvstlsfstype-asnvstfcvlglesmklpslpynle----- 235
QY      243  PDHWPITAVLPVLIICVWFCLILWKMKKKRPRNSYKCGTNTMERRESEOTKKREKIH 302
Db      236  -----tnkverkesegltkeirvyn 254
QY      303  IPEKSPDEAQRVFKSKSTSCDKSDTCF 329
Db      255  etersdaqcv-nisktaasdnstqf 280

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